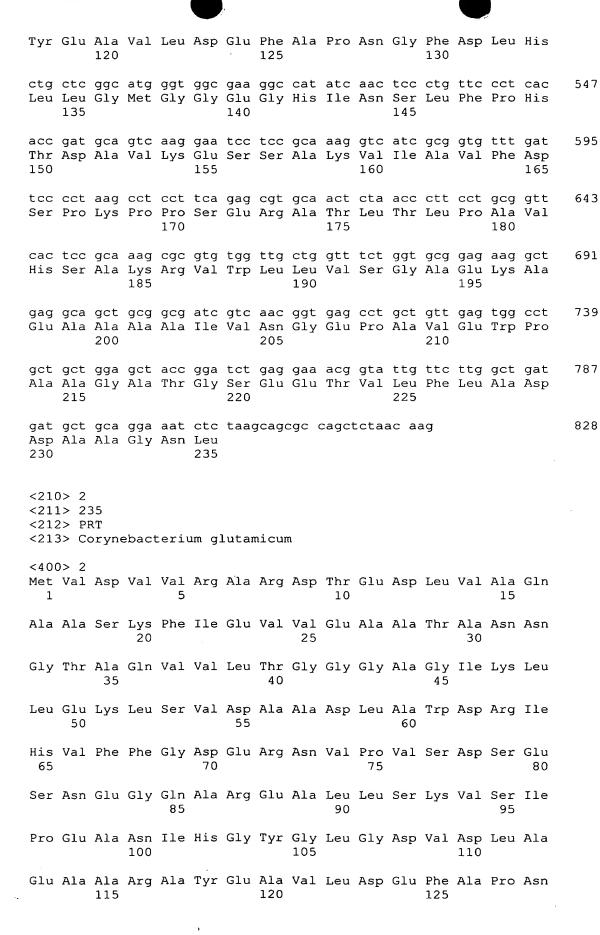
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<110> Pompejus, Markus Kroger, Burkhard Schroder, Hartwig Zelder, Oskar Haberhauer, Gregor <120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN CARBON METABOLISM AND ENERGY PRODUCTION <130> BGI 126CP <141/> <1/60> /182 <210 > 1 <2/1> 828 <2/12> DNA ₹213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(805) <223> RXS02735 <400> 1 gaggagette gecaeatgga tecagatttg ggetaecage aegeaetate eggettqtee 60 agcgtcaagc tggaaaccgt ctaaggagaa atacaacact atg gtt gat gta gta Met Val Asp Val Val cgc gca cgc gat act gaa gat ttg gtt gca cag gct gcc tcc aaa ttc Arg Ala Arg Asp Thr Glu Asp Leu Val Ala Gln Ala Ala Ser Lys Phe att gag gtt gtt gaa gca gca act gcc aat aat ggc /cc gca cag gta 211 Ile Glu Val Val Glu Ala Ala Thr Ala Asn Asn Gly Thr Ala Gln Val gtg ctc acc ggt ggt ggc gcc ggc atc aag tyg ctg gaa aag ctc agc 259 Val Leu Thr Gly Gly Gly Ala Gly Ile Lys Leu Leu Glu Lys Leu Ser 45 gtt gat gcg gct gac ctt gcc tgg gat cgc att cat gtg ttc ttc ggc 307 Val Asp Ala Ala Asp Leu Ala Trp Asp Arg Ile His Val Phe Phe Gly 60 gat gag cgc aat gtc cct gtc agt gat tct gag tcc aat gag ggc cag 355 Asp Glu Arg Asn Val Pro Val Ser Asp Ser Glu Ser Asn Glu Gly Gln 80 gct cgt gag gca /tg ttg tcc aag gtt tct atc cct gaa gcc aac att 403 Ala Arg Glu Ala Leu Leu Ser Lys Val Ser Ile Pro Glu Ala Asn Ile cac gga tax ggt ctc ggc gac gta gat ctt gca gag gca gcc cgc gct 451 His Gly T√r Gly Leu Gly Asp Val Asp Leu Ala Glu Ala Ala Arg Ala tac gaa got gtg ttg gat gaa tto goa coa aac ggo ttt gat ott cac 499



Gly Phe Asp Leu His Leu Leu Gly Met Gly Glu Gly His Ile Asn 130 135 Ser Leu Phe Pro His Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val Ile Ala Val Phe Asp Ser Pro Lys Pro Pro Ser Glu Arg Ala Thr Leu Thr Leu Pro Ala Val His Ser Ala Lys Arg Val Trp Leu Leu Val Ser 185 Gly Ala Glu Lys Ala Glu Ala Ala Ala Ile Val Asn Gly Glu Pro Ala Val Glu Trp Pro Ala Ala Gly Ala Thr Gly Ser Glu Glu Thr Val 215 Leu Phe Leu Ala Asp Asp Ala Ala Gly Asn Leu 230 <210> 3 <211> 468 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(445) <223> RXA01626 <400> 3 gcaatagcga atgcgtaatt aaccacactt caaacctagc ccctcaggtg gaggattccg 60 acattaccgt ctgaaaaatt tcatccgtag gctaaagagc atg tcg aaa acg atc 115 Met Ser Lys Thr Ile atc gtg cgc acc gaa att gaa atc cct gga cac cca acc gcc atc cat 163 Ile Val Arg Thr Glu Ile Glu Ile Pro Gly His Pro Thr Ala Ile His 10 15 atc gca gag atg cag gag ctt ccc cca tct gag gct caa ggc ggc gtg 211 Ile Ala Glu Met Gln Glu Leu Pro Pro Ser Glu Ala Gln Gly Gly Val 30 cag atg tgc aaa atg cag cgc att att gaa cta gca gga act gcc gaa 259 Gln Met Cys Lys Met Gln Arg Ile Ile Glu Leu Ala Gly Thr Ala Glu 45 ggg gat gtc gtt act ggt gca ggt gtt att ggc gga tct aat ttc cag 307 Gly Asp Val Val Thr Gly Ala Gly Val Ile Gly Gly Ser Asn Phe Gln 60 ctg aat aac gag cca aat gaa gtg gtt ccc cat cca gat acc tat gcg 355 Leu Asn Asn Glu Pro Asn Glu Val Val Pro His Pro Asp Thr Tyr Ala 75 gat ttc ccc gat atc aag gcg gtt gtt atc tcc gcg gag act ttt gaa 403



Asp Phe Pro Asp Ile Lys Ala Val Val Ile Ser Ala Glu Thr Phe Glu 90 95 445 ggc ctg tgg ctg gaa gcg gga gcg aag ttc cct ggg tta aat Gly Leu Trp Leu Glu Ala Gly Ala Lys Phe Pro Gly Leu Asn 110 taaccacttg cagtataccc tag 468 <210> 4 <211> 115 <212> PRT <213> Corynebacterium glutamicum <400> 4 Met Ser Lys Thr Ile Ile Val Arg Thr Glu Ile Glu Ile Pro Gly His 10 Pro Thr Ala Ile His Ile Ala Glu Met Gln Glu Leu Pro Pro Ser Glu Ala Gln Gly Val Gln Met Cys Lys Met Gln Arg Ile Ile Glu Leu Ala Gly Thr Ala Glu Gly Asp Val Thr Gly Ala Gly Val Ile Gly Gly Ser Asn Phe Gln Leu Asn Asn Glu Pro Asn Glu Val Val Pro His Pro Asp Thr Tyr Ala Asp Phe Pro Asp Ile Lys Ala Val Val Ile Ser Ala Glu Thr Phe Glu Gly Leu Trp Leu Glu Ala Gly Ala Lys Phe Pro 105 Gly Leu Asn 115 <210> 5 <211> 780 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(757) <223> RXA02245 gccacaccgc cacggcaccg atgcgatgtt tgtggcagtg ctgcgaaaga agtagacctg 60 tgagctaagt ggggtagaca agagggctat gatttagggc atg gca caa cgt act 115 Met Ala Gln Arg Thr cca cta atc gcc cca tcc att ctt gct gct gat ttc tcc cgc tta ggg 163

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10

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Arg	Lys	Val	Ile	Asp 165	Glu	Arg	Gly	Leu	Asn 170	Thr	Val	Ile	Glu	Ile 175	Asp	
Gly	Gly	Ile	Ser 180	Ala	Lys	Thr	Ile	Lys 185	Gln	Ala	Ala	Asp	Ala 190	Gly	Val	
Asp	Ala	Phe 195	Val	Ala	Gly	Ser	Ala 200	Val	Tyr	Gly	Ala	Glu 205	Asp	Pro	Asn	
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tato	ccgc	cgt t	igtga	aaaat	ig co	ctgca	agtaa	a act	gact	tcc				tac Tyr		115
		gac Asp														163

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gtc tca gct g Val Ser Ala G						
acc aaa gat a Thr Lys Asp M 40						
cca ctg aac c Pro Leu Asn A 55			_			_
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aag gcg ttc a Lys Ala Phe T	-	-		-		-
gca cag ggt g Ala Gln Gly G 1						
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ggt cgc gag t Gly Arg Glu S 135	er Asp Cys 1					
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2

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	cgc Arg															1699
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	ggc Gly															1795
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Pro Ala Gly Val Pro Thr Lys Asp Met Trp Glu Tyr Gln Lys Asp His
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Met Asn Leu Val Ser Pro Leu Asn Arg Arg Lys Phe Arg Val Leu Val 50 55 60

Val Gly Thr Gly Leu Ser Gly Gly Ala Ala Ala Ala Leu Gly Glu 65 70 75 80

Leu Gly Tyr Asp Val Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg 85 90 95

Ala His Ser Ile Ala Ala Gln Gly Gly Val Asn Ser Ala Arg Gly Lys 100 105 110

Lys Val Asp Asn Asp Gly Ala Tyr Arg His Val Lys Asp Thr Val Lys 115 120 125

Gly Gly Asp Tyr Arg Gly Arg Glu Ser Asp Cys Trp Arg Leu Ala Val 130 135 140

Glu Ser Val Arg Val Ile Asp His Met Asn Ala Ile Gly Ala Pro Phe 145 150 155 160

Ala Arg Glu Tyr Gly Gly Ala Leu Ala Thr Arg Ser Phe Gly Gly Val 165 170 175

Gln Val Ser Arg Thr Tyr Tyr Thr Arg Gly Gln Thr Gly Gln Gln Leu 180 185 190

Gln Phe Ser Thr Ala Ser Ala Leu Gln Arg Gln Ile His Leu Gly Ser 195 200 205

Val Glu Ile Phe Thr His Asn Glu Met Val Asp Val Ile Val Thr Glu 210 215 220

Arg Asn Gly Glu Lys Arg Cys Glu Gly Leu Ile Met Arg Asn Leu Ile 225 230 235 240

Thr Gly Glu Leu Thr Ala His Thr Gly His Ala Val Ile Leu Ala Thr 245 250 255

Gly Gly Tyr Gly Asn Val Tyr His Met Ser Thr Leu Ala Lys Asn Ser 260 265 270

Asn Ala Ser Ala Ile Met Arg Ala Tyr Glu Ala Gly Ala Tyr Phe Ala 275 280 285

595

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Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly Ala His Phe Arg Asp Asp His Leu Ser Glu Asp Gly Glu Ala Gln Arg Asp Asp Gln Asn Trp Cys 630 Phe Val Ser Ala Trp Glu Pro Gly Glu Asn Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe Phe Glu Ser Val Pro Leu Gln Thr Arg Asn Tyr 665 Lys <210> 11 <211> 1100 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(1077) <223> FRXA01312 <400> 11 gag tcg ctg cgt aac gac ggc cgc atc tgg tcc cct aag gaa ccg aac 48 Glu Ser Leu Arg Asn Asp Gly Arg Ile Trp Ser Pro Lys Glu Pro Asn gat aac ege gat eea aac ace ate eet gag gat gag ege gae tae tte 96 Asp Asn Arg Asp Pro Asn Thr Ile Pro Glu Asp Glu Arg Asp Tyr Phe 20 25 ctg gag cgc cgc tac cca gca ttc ggt aac ctc gtc cca cgt gac gtt 144 Leu Glu Arg Arg Tyr Pro Ala Phe Gly Asn Leu Val Pro Arg Asp Val 40 get tee egt geg ate tee eag eag ate aat get ggt ete ggt gtt gga 192 Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala Gly Leu Gly Val Gly 50 55 cct ctg aac aac gct gca tac ctg gac ttc cgc gac gcc acc gag cgc 240 Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg 65 70 ctc gga cag gac acc atc cgc gag cgt tac tcc aac ctc ttc acc atg 288 Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met 85 90 tac gaa gag gca att ggc gag gac cca tac tcc agc cca atg cgt att 336 Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile 100 105 110 gca ccg acc tgc cac ttc acc atg ggt ggc ctc tgg act gac ttc aac 384 Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu Trp Thr Asp Phe Asn 115 120

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Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp

432

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Ala Ser Arg Ala Ile Ser Gln Gln Ile Asn Ala Gly Leu Gly Val Gly 50 55 60

Pro Leu Asn Asn Ala Ala Tyr Leu Asp Phe Arg Asp Ala Thr Glu Arg 65 70 75 80

Leu Gly Gln Asp Thr Ile Arg Glu Arg Tyr Ser Asn Leu Phe Thr Met 85 90 95

Tyr Glu Glu Ala Ile Gly Glu Asp Pro Tyr Ser Ser Pro Met Arg Ile 100 105 110

Ala Pro Thr Cys His Phe Thr Met Gly Gly Leu Trp Thr Asp Phe Asn 115 120 125

Glu Met Thr Ser Leu Pro Gly Leu Phe Cys Ala Gly Glu Ala Ser Trp 130 135 140

Thr Tyr His Gly Ala Asn Arg Leu Gly Ala Asn Ser Leu Leu Ser Ala 145 150 155 160

Ser Val Asp Gly Trp Phe Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu 165 170 175

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Gln Ala Ala Ile Ala Arg Ala Gln Ala Arg Ile Asp Arg Leu Met Gly
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His Arg Gln Leu Gly Asp Ile Leu Tyr Phe Ser Cys Gly Val Ser Arg 225 230 235 240

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Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly Ser Thr Asp Glu Met 260 265 270

Asn Gln Val Leu Glu Tyr Ala Ala Arg Val Ala Asp Tyr Ile Asp Leu 275 280 285

Gly Glu Leu Met Cys Val Asp Ala Leu Asp Arg Asp Glu Ser Cys Gly 290 295 300

Ala His Phe Arg Asp Asp His Leu Ser Glu Asp Gly Glu Ala Gln Arg 310 Asp Asp Gln Asn Trp Cys Phe Val Ser Ala Trp Glu Pro Gly Glu Asn 325 330 Gly Thr Phe Val Cys His Ala Glu Pro Leu Phe Phe Glu Ser Val Pro 345 Leu Gln Thr Arg Asn Tyr Lys 355 <210> 13 <211> 1593 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1570) <223> RXN00231 <400> 13 caggactace tegacgeegg egecaacttt gteegagteg gtgeegatgt eeageaacte 60 aacgctgctg gatacgaaaa gtgaaggaaa ataacgcatc atg act att aat gtt Met Thr Ile Asn Val 5 tto gaa cta ctt gtc aaa agt ccc acg ggt cta ctg att ggt gat tcc 163 Phe Glu Leu Leu Val Lys Ser Pro Thr Gly Leu Leu Ile Gly Asp Ser tgg gtg gaa gca tee gae gge ggt aet tte gat gtg gaa aae eea geg 211 Trp Val Glu Ala Ser Asp Gly Gly Thr Phe Asp Val Glu Asn Pro Ala 25 acg ggt gaa aca atc gca acg ctc gcg tct gct act tcc gag gat gca 259 Thr Gly Glu Thr Ile Ala Thr Leu Ala Ser Ala Thr Ser Glu Asp Ala ctg gct gct ctt gat gct gca tgc gct gtt cag gcc gag tgg gct agg 307 Leu Ala Ala Leu Asp Ala Ala Cys Ala Val Gln Ala Glu Trp Ala Arg atg cca gcg cgc gag cgt tct aat att tta cgc cgc ggt ttt gag ctc 355 Met Pro Ala Arg Glu Arg Ser Asn Ile Leu Arg Arg Gly Phe Glu Leu gta gca gaa cgt gca gaa gag ttc gcc acc ctc atg acc ttg gaa atg 403 Val Ala Glu Arg Ala Glu Glu Phe Ala Thr Leu Met Thr Leu Glu Met 90 95 ggc aag cct ttg gct gaa gct cgc ggc gaa gtc acc tac ggc aac gaa 451 Gly Lys Pro Leu Ala Glu Ala Arg Gly Glu Val Thr Tyr Gly Asn Glu 105 . 110

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130

125

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Thr Ser Glu Asp Ala Leu Ala Ala Leu Asp Ala Ala Cys Ala Val Gln 50 55 60

Ala Glu Trp Ala Arg Met Pro Ala Arg Glu Arg Ser Asn Ile Leu Arg 65 70 75 80

Arg Gly Phe Glu Leu Val Ala Glu Arg Ala Glu Glu Phe Ala Thr Leu 85 90 95

Met Thr Leu Glu Met Gly Lys Pro Leu Ala Glu Ala Arg Gly Glu Val 100 105 110

Thr Tyr Gly Asn Glu Phe Leu Arg Trp Phe Ser Glu Glu Ala Val Arg

120 125 115 Leu Tyr Gly Arg Tyr Gly Thr Thr Pro Glu Gly Asn Leu Arg Met Leu 135 Thr Ala Leu Lys Pro Val Gly Pro Cys Leu Leu Ile Thr Pro Trp Asn 155 Phe Pro Leu Ala Met Ala Thr Arg Lys Val Ala Pro Ala Ile Ala Ala Gly Cys Val Met Val Leu Lys Pro Ala Arg Leu Thr Pro Leu Thr Ser Gln Tyr Phe Ala Gln Thr Met Leu Asp Ala Gly Leu Pro Ala Gly Val Leu Asn Val Val Ser Gly Ala Ser Ala Ser Ala Ile Ser Asn Pro Ile 215 Met Glu Asp Asp Arg Leu Arg Lys Val Ser Phe Thr Gly Ser Thr Pro 235 Val Gly Gln Gln Leu Leu Lys Lys Ala Ala Asp Lys Val Leu Arg Thr Ser Met Glu Leu Gly Gly Asn Ala Pro Phe Ile Val Phe Glu Asp Ala 265 Asp Leu Asp Leu Ala Ile Glu Gly Ala Met Gly Ala Lys Met Arg Asn 280 Ile Gly Glu Ala Cys Thr Ala Ala Asn Arg Phe Leu Val His Glu Ser 295 Val Ala Asp Glu Phe Gly Arg Arg Phe Ala Ala Arg Leu Glu Gln 315 Val Leu Gly Asn Gly Leu Asp Glu Gly Val Thr Val Gly Pro Leu Val Glu Glu Lys Ala Arg Asp Ser Val Ala Ser Leu Val Asp Ala Ala Val Ala Glu Gly Ala Thr Val Leu Thr Gly Gly Lys Ala Gly Thr Gly Ala Gly Tyr Phe Tyr Glu Pro Thr Val Leu Thr Gly Val Ser Thr Asp Ala Ala Ile Leu Asn Glu Glu Ile Phe Gly Pro Val Ala Pro Ile Val Thr Phe Gln Thr Glu Glu Glu Ala Leu Arg Leu Ala Asn Ser Thr Glu Tyr 405 410 Gly Leu Ala Ser Tyr Val Phe Thr Gln Asp Thr Ser Arg Ile Phe Arg 420 425 Val Ser Asp Gly Leu Glu Phe Gly Leu Val Gly Val Asn Ser Gly Val 435 440 445

Ile Ser Asn Ala Ala Pro Phe Gly Gly Val Lys Gln Ser Gly Met 450 455 Gly Arg Glu Gly Gly Leu Glu Gly Ile Glu Glu Tyr Thr Ser Val Gln 475 Tyr Ile Gly Ile Arg Asp Pro Tyr Ala Gly 485 <210> 15 <211> 870 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(847) <223> RXA01311 <400> 15 tegteteege atgggaacca ggegagaatg gaacettegt etgeeaegea gaaceaetgt 60 tcttcgaatc tgtcccactg cagacaagga actacaagta atg aaa ctt aca ctt 115 Met Lys Leu Thr Leu 1 gag atc tgg cgt caa gca ggc cca act gcg gaa ggc aag ttc gaa acc 163Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr 10 gtc cag gtt gac gac gcc gtc gcg cag atg tcc atc ctg gag ctg ctt 211 Val Gln Val Asp Asp Ala Val Ala Gln Met Ser Ile Leu Glu Leu Leu 25 259 gac cac gta aac aac aag ttc atc gaa gaa ggc aaa gaa cca ttc gcg Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala ttc gcc tct gac tgc cgc gaa ggc att tgt ggt acc tgt ggt ctc ctc 307 Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu 55 gtg aac ggt cgc cct cac ggc gcc gac cag aac aag cct gcc tgt gcg 355 Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala 403 cag cgc ctg gtc agc tac aag gaa ggc gac acc ctc aag atc gaa cca Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro ctg cgt tcc gcc gca tac cca gtg atc aag gac atg gtc gtc gac cgc 451 Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg 110 tcc gca ctg gac cgt gtc atg gaa cag ggt ggc tac gtg acc atc aac 499 Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly Tyr Val Thr Ile Asn

125

gca ggt acc gca cct gac gct gat acc ctc cac gtc aac cac gaa acc

547

1

Ala	Gly 135	Thr	Ala	Pro	Asp	Ala 140	Asp	Thr	Leu	His	Val 145	Asn	His	Glu	Thr	
_	-		-		gac Asp 155		_	_	_			_		_	_	595
-	_	-	_		aac Asn		-	_		_				_	_	643
					ctc Leu											693
					gtt Val											739
					tgc Cys	-	-	_	_		-				_	787
	_		_	_	gtc Val 235		_	_	-		_	-	_		_	835
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<213> Corynebacterium glutamicum

<400> 16

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Gly Lys Phe Glu Thr Val Gln Val Asp Asp Ala Val Ala Gln Met Ser 20 25 30

Ile Leu Glu Leu Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly 35 40 45

Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly 50 55 60

Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn 65 70 75 80

Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr 85 90 95

Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp 100 105 110

Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly 115 120 125

Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His 130 135 Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile 155 Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu 170 Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys 185 Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr 200 Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro 215 Ala Gly Ile Pro Leu Thr Ala Val Ala Ala Val Thr Lys Glu Arq Ala Arg Ala Ala Phe Arg Gly Lys Asp Asp 245 <210> 17 <211> 1530 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1507) <223> RXA01535 <400> 17 acceaectea etetaggggt ggaeteeagt gtttegegae aacacaatga gtaagettgt 60 gacagccgta tttaattctc agtaagaaat gagtgatttc atg acc gag cag gaa 115 Met Thr Glu Gln Glu ttc cgt att gag cac gac acc atg ggt gaa gtg aag gtt cca gca aag 163 Phe Arg Ile Glu His Asp Thr Met Gly Glu Val Lys Val Pro Ala Lys 10 15 gct ctg tgg cag gca cag acc cag cgc gct gtt gag aac ttc cct atc 211 Ala Leu Trp Gln Ala Gln Thr Gln Arg Ala Val Glu Asn Phe Pro Ile 25 30 259 tot ggt cgt ggt ctg gaa too goa cag ato cgc gca atg ggt ctg ctg Ser Gly Arg Gly Leu Glu Ser Ala Gln Ile Arg Ala Met Gly Leu Leu 40 aag gca gct tgt gcg cag gta aac aag gac tcc ggt gcg ctg gat gca 307 Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser Gly Ala Leu Asp Ala 55 gag aag gca gat gcc atc att gca gct ggt aag gag atc gcg tcc ggt 355 Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys Glu Ile Ala Ser Gly

70					75					80					85	
						cca Pro										403
				_		acc Thr			-		_				-	451
_			_		_	cac His			_		-		_		_	499
			_			cct Pro 140		_			_	_	_		-	547
_	_	_		_		atc Ile			_	_	_	_				595
_		_	_	_		gag Glu				_	_	_			-	643
						gtt Val										691
		_	_	_		cag Gln					_	_		_		739
						ctg Leu 220										787
					-	gat Asp										835
		_		_	_	aag Lys			_	_	_					883
	_	_	_	_	_	gac Asp	_		_					_	_	931
_	-		-	_		ttg Leu		_		-		_		_		979
_					-	acc Thr 300						-			-	1027
						atc Ile										1075

tgt gag acc Cys Glu Thr											1123
gct gtt gcg Ala Val Ala				/ Gln							1171
atc cca gtg Ile Pro Val 360		-				_	_	_	_	_	1219
aac act tcc Asn Thr Ser 375		_	_		_	_					1267
aac gag gca Asn Glu Ala 390	_		_							_	1315
acc cca ctg Thr Pro Leu											1363
aag act gct Lys Thr Ala			_	: Ile	_	_		_		-	1411
ttg ggc ttg Leu Gly Leu 440			-			_		-	-	_	1459
cgc ctc gac Arg Leu Asp 455											1507
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Glu Asn Phe 35	Pro Ile	Ser Gly	Arg Gly	/ Leu	Glu	Ser	Ala 45	Gln	Ile	Arg	
Ala Met Gly 50	Leu Leu	Lys Ala 55	Ala Cys	Ala	Gln	Val 60	Asn	Lys	Asp	Ser	
Gly Ala Leu 65	Asp Ala	Glu Lys 70	Ala Asp	Ala	Ile 75	Ile	Ala	Ala	Gly	Lys 80	

Glu Ile Ala Ser Gly Lys His Asp Ala Glu Phe Pro Ile Asp Val Phe Gln Thr Gly Ser Gly Thr Ser Ser Asn Met Asn Thr Asn Glu Val Ile 105 Ala Ser Ile Ala Lys Ala Asn Gly Val Glu Val His Pro Asn Asp His 120 Val Asn Met Gly Gln Ser Ser Asn Asp Thr Phe Pro Thr Ala Thr His 130 135 Val Ala Ala Thr Glu Ala Ala Val Asn Asp Leu Ile Pro Gly Leu Lys Val Leu His Glu Ser Leu Ala Lys Lys Ala Asn Glu Trp Ser Glu Val Val Lys Ser Gly Arg Thr His Leu Met Asp Ala Val Pro Val Thr Leu 185 Gly Gln Glu Phe Gly Gly Tyr Ala Arg Gln Ile Gln Leu Gly Ile Glu Arg Val Glu Ala Thr Leu Pro Arg Leu Gly Glu Leu Ala Ile Gly Gly Thr Ala Ala Gly Thr Gly Ile Asn Thr Ser Ala Asp Phe Gly Gly Lys Val Val Ala Glu Leu Ile Asn Leu Thr Asp Val Lys Glu Leu Lys Glu Ala Glu Asn His Phe Glu Ala Gln Ala Ala Arg Asp Ala Leu Val Glu Phe Ser Gly Ala Met Arg Val Ile Ala Val Ser Leu Tyr Lys Ile Ala Asn Asp Ile Arg Leu Met Gly Ser Gly Pro Leu Thr Gly Leu Gly Glu 295 Ile Arg Leu Pro Asp Leu Gln Pro Gly Ser Ser Ile Met Pro Gly Lys 310 315 Val Asn Pro Val Leu Cys Glu Thr Ala Thr Gln Val Ser Ala Gln Val 330 Ile Gly Asn Asp Ala Ala Val Ala Phe Ser Gly Thr Gln Gly Gln Phe Glu Leu Asn Val Phe Ile Pro Val Met Ala Arg Asn Val Leu Glu Ser Ala Arg Leu Leu Ala Asn Thr Ser Arg Val Phe Ala Thr Arg Leu Val 375 Asp Gly Ile Glu Pro Asn Glu Ala His Met Lys Glu Leu Ala Glu Ser 390 395

Ser Pro Ser Ile Val Thr Pro Leu Asn Ser Ala Ile Gly Tyr Glu Ala

405 410 415 Ala Ala Lys Val Ala Lys Thr Ala Leu Ala Glu Gly Lys Thr Ile Arg 425 Gln Thr Val Ile Asp Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu 435 445 Glu Glu Leu Asp Lys Arg Leu Asp Val Leu Ala Met Ala His Thr Glu Arg Glu Asn Lys Phe 465 <210> 19 <211> 1164 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1141) <223> RXA00517 <400> 19 ggtcttagaa ccagcgtgca ctgatggcga ttaaaggggg ttgcgcctat acctattgct 60 ggtatacatt tcggtatacc taaaccgaat tgagggattc atg cca gaa gtc act 115 Met Pro Glu Val Thr gtc aac gcc caa caa ctc act gtt ctc tgc aca gac atc ctc acc aaa 163 Val Asn Ala Gln Gln Leu Thr Val Leu Cys Thr Asp Ile Leu Thr Lys 10 act gga gta cct gca gca gac gcc cat ctt gtc ggt gat agt ttg gtg 211 Thr Gly Val Pro Ala Ala Asp Ala His Leu Val Gly Asp Ser Leu Val 25 cag gct gat ctt tgg ggt cac ccc tcc cac ggt gtg ctt cga ctg cct 259 Gln Ala Asp Leu Trp Gly His Pro Ser His Gly Val Leu Arg Leu Pro 40 tgg tat gtg cgc aga ctc cac agt ggc gcg atg act aca cat gca cac 307 Trp Tyr Val Arg Arg Leu His Ser Gly Ala Met Thr Thr His Ala His gtg gag gtt ctc aat gat ttg ggt gcc gtg ttg gcg ttg gat gga cac 355 Val Glu Val Leu Asn Asp Leu Gly Ala Val Leu Ala Leu Asp Gly His aat gga atc ggc caa gtt tta gct gat cat gct cgt aaa gaa gca gtg 403 Asn Gly Ile Gly Gln Val Leu Ala Asp His Ala Arg Lys Glu Ala Val 90 95 act agg gca atg atg ttc ggc atc ggt gcg gtg tcg gtg cgc aac tcc 451 Thr Arg Ala Met Met Phe Gly Ile Gly Ala Val Ser Val Arg Asn Ser 105 110 aat cat ttt gga act gcc atg tac tac acc cgg aaa gcg gca gcg caa 499

Asn	His	Phe 120	Gly	Thr	Ala	Met	Tyr 125	Tyr	Thr	Arg	Lys	Ala 130	Ala	Ala	Gln	
_						acc Thr 140			-		_					547
						cgg Arg										595
						gct Ala										643
_		_		_		tac Tyr		_	_	_			_			691
						acg Thr	_			_			_	_		739
_		_				gtc Val 220	_				_					787
						atg Met										835
						gta Val										883
		-			-	ttc Phe			_		_	_				931
						gac Asp										979
			_		_	caa Gln 300										1027
-	_	_	_	_		cat His										1075
						atg Met										1123
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<213> Corynebacterium glutamicum

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Asp Ile Leu Thr Lys Thr Gly Val Pro Ala Ala Asp Ala His Leu Val 20 25 30

Gly Asp Ser Leu Val Gln Ala Asp Leu Trp Gly His Pro Ser His Gly
35 40 45

Val Leu Arg Leu Pro Trp Tyr Val Arg Arg Leu His Ser Gly Ala Met 50 55 60

Thr Thr His Ala His Val Glu Val Leu Asn Asp Leu Gly Ala Val Leu 65 70 75 80

Ala Leu Asp Gly His Asn Gly Ile Gly Gln Val Leu Ala Asp His Ala 85 90 95

Arg Lys Glu Ala Val Thr Arg Ala Met Met Phe Gly Ile Gly Ala Val 100 105 110

Ser Val Arg Asn Ser Asn His Phe Gly Thr Ala Met Tyr Tyr Thr Arg 115 120 125

Lys Ala Ala Ala Gln Gly Cys Val Ser Ile Leu Thr Thr Asn Ala Ser 130 135 140

Pro Ala Met Ala Pro Trp Gly Gly Arg Glu Lys Arg Ile Gly Thr Asn 145 150 155 160

Pro Trp Ser Ile Ala Ala Pro Phe Gly Glu Thr Ala Thr Val Val Asp 165 170 175

Ile Ala Asn Thr Ala Val Ala Arg Gly Lys Ile Tyr His Ala Arg Gln 180 185 190

Thr Asn Met Pro Ile Pro Glu Thr Trp Ala Ile Thr Ser Glu Gly Ala 195 200 205

Pro Thr Thr Asp Pro Ala Glu Ala Ile Asn Gly Val Val Leu Pro Met 210 215 220

Ala Gly His Lys Gly Tyr Ala Ile Ser Phe Met Met Asp Val Leu Ser 225 230 235 240

Gly Val Leu Thr Gly Ser Gln His Ser Thr Lys Val His Gly Pro Tyr 245 250 255

Asp Pro Thr Pro Pro Gly Gly Ala Gly His Leu Phe Ile Ala Leu Asp 260 265 270

Val Ala Ala Phe Arg Asp Pro Gln Asp Phe Asp Asp Ala Leu Ser Asp 275 280 285

Leu Val Gly Glu Val Lys Ser Thr Pro Lys Ala Gln Asn Thr Glu Glu 290 295 300

Ile Phe Tyr Pro Gly Glu Ser Glu Asp Arg Ala His Arg Lys Asn Ser305310315320Ala His Gly Ile Ser Leu Pro Glu Lys Thr Trp Met Glu Leu Gln Glu325330335

Leu Ala Ile Glu Asn His Val Val Thr His Arg 340 345

<210> 21

<211> 1107

<212> DNA

<213> Corynebacterium glutamicum

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ggttcttaga ggacccccta caaggattga ggattgttta atg aat tcc ccg cag 115

Met Asn Ser Pro Gln

1 5

aac gtc tcc acc aag aag gtc acc gtc acc ggc gca gct ggt caa atc 163 Asn Val Ser Thr Lys Lys Val Thr Val Thr Gly Ala Ala Gly Gln Ile 10 15 20

tet tat tea etg ttg tgg ege ate gee aac ggt gaa gta tte gge acc 211 Ser Tyr Ser Leu Leu Trp Arg Ile Ala Asn Gly Glu Val Phe Gly Thr 25 30 35

gac acc cct gta gaa ctg aaa ctt ctg gag atc cct cag gct ctt ggc 259
Asp Thr Pro Val Glu Leu Lys Leu Glu Ile Pro Gln Ala Leu Gly
40 45 50

ggg gca gag ggt gtg gct atg gaa ctt ctg gat tct gcc ttc ccc ctc 307 Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp Ser Ala Phe Pro Leu 55 60 65

ctg cga aac atc acc acc gcg gat gcc aat gag gca ttc gac ggc 355 Leu Arg Asn Ile Thr Ile Thr Ala Asp Ala Asn Glu Ala Phe Asp Gly 70 75 80 85

gct aat gcg gcg ttt ttg gtc ggt gcg aag cct cgc gga aaa ggc gaa 403 Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro Arg Gly Lys Gly Glu

gag cgc gca gat ttg ctg gct aac aac ggc aag att ttc gga cct caa 451 Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys Ile Phe Gly Pro Gln 105 110 115

ggt aaa gct atc aat gac aac gcc gca gat gac att cgt gtc cta gtt 499 Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp Ile Arg Val Leu Val 120 125 130

gtt gga aac cca gcg aac acc aac gcg ttg att gct tca gct gcg gcc 547

Val	Gly 135	Asn	Pro	Ala	Asn	Thr 140	Asn	Ala	Leu	Ile	Ala 145	Ser	Ala	Ala	Ala	
		gtt Val				_								_		595
		gcg Ala														643
		aac Asn														691
		atc Ile 200														739
		cac His														787
		gct Ala														835
_	_	tcc Ser				_		_	_			_	_			883
		tgg Trp														931
		ggc Gly 280			_		_			_		_				979
	-	atc Ile	_	_		-				-		_	_	_	_	1027
	_	gcg Ala		_	_	_	-	_	_		-		-		_	1075
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<210> 22

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 22

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Glu Val Phe Gly Thr Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile 35 40 45

Pro Gln Ala Leu Gly Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp 50 55 60

Ser Ala Phe Pro Leu Leu Arg Asn Ile Thr Ile Thr Ala Asp Ala Asn 65 70 75 80

Glu Ala Phe Asp Gly Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro 85 90 95

Arg Gly Lys Gly Glu Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys 100 105 110

Ile Phe Gly Pro Gl
n Gly Lys Ala Ile As
n Asp As
n Ala Ala Asp Asp 115 120 125

Ile Arg Val Leu Val Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile 130 135 140

Ala Ser Ala Ala Ala Pro Asp Val Pro Ala Ser Arg Phe Asn Ala Met 145 150 155 160

Met Arg Leu Asp His Asn Arg Ala Ile Ser Gln Leu Ala Thr Lys Leu 165 170 175

Gly Arg Gly Ser Ala Glu Phe Asn Asn Ile Val Val Trp Gly Asn His 180 185 190

Ser Ala Thr Gln Phe Pro Asp Ile Thr Tyr Ala Thr Val Gly Glu 195 200 205

Lys Val Thr Asp Leu Val Asp His Asp Trp Tyr Val Glu Glu Phe Ile 210 215 220

Pro Arg Val Ala Asn Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys 225 230 235 240

Ser Ser Ala Ala Ser Ala Ala Ser Ser Ala Ile Asp His Met Arg Asp 245 250 255

Trp Val Gln Gly Thr Glu Ala Trp Ser Ser Ala Ala Ile Pro Ser Thr 260 265 270

Gly Ala Tyr Gly Ile Pro Glu Gly Ile Phe Val Gly Leu Pro Thr Val 275 280 285

Ser Arg Asn Gly Glu Trp Glu Ile Val Glu Gly Leu Glu Ile Ser Asp 290 295 300

Phe Gln Arg Ala Arg Ile Asp Ala Asn Ala Gln Glu Leu Gln Ala Glu 305 310 315 320

Arg Glu Ala Val Arg Asp Leu Leu 325

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<211> 1092
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<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(1069)
<223> RXA02149
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aattcaccta aatcctgtgt agaacgcgag gggcactctt atg cca caa aaa ccg
                                                                    115
                                             Met Pro Gln Lys Pro
                                                                    163
gcc agt ttc gcg gtg ggc ttt gac atc ggc ggc acc aac atg cga gcc
Ala Ser Phe Ala Val Gly Phe Asp Ile Gly Gly Thr Asn Met Arg Ala
                                      15
                                                                    211
ggg ctt gtc gac gaa tcc ggg cgc atc gtg acc agt ttg tcg gcg ccg
Gly Leu Val Asp Glu Ser Gly Arg Ile Val Thr Ser Leu Ser Ala Pro
             25
                                  30
                                                                    259
tcg ccg cgc acg acg cag gca atg gaa cag ggg att ttt gat cta gtc
Ser Pro Arg Thr Thr Gln Ala Met Glu Gln Gly Ile Phe Asp Leu Val
         40
                              4.5
                                                                    307
gaa cag etc aag gee gaa tae eeg gtt ggt get gtg gga ett gee gte
Glu Gln Leu Lys Ala Glu Tyr Pro Val Gly Ala Val Gly Leu Ala Val
                          60
gcq qga ttt ttg gat cct qag tgc gag gtt gtt cga ttt gcc ccg cac
                                                                    355
Ala Gly Phe Leu Asp Pro Glu Cys Glu Val Val Arg Phe Ala Pro His
 70
ctt cct tgg cgc gat gag cca gtg cgt gaa aag ttg gaa aac ctt ttg
                                                                    403
Leu Pro Trp Arg Asp Glu Pro Val Arg Glu Lys Leu Glu Asn Leu Leu
                 90
                                      95
ggc ctg cct gtt cgt ttg gaa cat gat gcc aac tca gca gcg tgg ggt
                                                                    451
Gly Leu Pro Val Arg Leu Glu His Asp Ala Asn Ser Ala Ala Trp Gly
            105
                                 110
gag cat cgt ttt ggt gca gct caa ggc gct gac aac tgg gtt ttg ttg
                                                                    499
Glu His Arg Phe Gly Ala Ala Gln Gly Ala Asp Asn Trp Val Leu Leu
        120
                             125
gca ctc ggc act gga att ggt gca gcg ctg att gaa aaa ggc gaa att
                                                                    547
Ala Leu Gly Thr Gly Ile Gly Ala Ala Leu Ile Glu Lys Gly Glu Ile
                         140
                                             145
    135
tac cgt ggt gca tat ggc acg gca cca gaa ttt ggt cat ttg cgt gtt
                                                                    595
Tyr Arg Gly Ala Tyr Gly Thr Ala Pro Glu Phe Gly His Leu Arg Val
150
                     155
                                         160
                                                              165
gtt cgt ggc gga cgc gca tgt gcg tgt ggc aaa gaa ggc tgc ctg gag
                                                                    643
Val Arg Gly Gly Arg Ala Cys Ala Cys Gly Lys Glu Gly Cys Leu Glu
                170
                                     175
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cgt tac tgt tcc ggt act gcc ttg gtt tac act gcg cgt gaa ttg gct 691 Arg Tyr Cys Ser Gly Thr Ala Leu Val Tyr Thr Ala Arg Glu Leu Ala 185 190 tcg cat ggc tca ttc cgc aac agc ggg ctg ttt gac aag atc aaa gcc 739 Ser His Gly Ser Phe Arg Asn Ser Gly Leu Phe Asp Lys Ile Lys Ala 200 205 gat ccg aat tcc atc aat gga aaa acg atc act gcg gca gcg cgc caa 787 Asp Pro Asn Ser Ile Asn Gly Lys Thr Ile Thr Ala Ala Ala Arg Gln 215 220 gaa gac cca ctt gct ctc gcc gtt ctg gaa gat ttc agc gag tgg ctg 835 Glu Asp Pro Leu Ala Leu Ala Val Leu Glu Asp Phe Ser Glu Trp Leu 230 235 883 ggc gaa act ttg gcg atc att gct gat gtc ctt gac cca ggc atg atc Gly Glu Thr Leu Ala Ile Ile Ala Asp Val Leu Asp Pro Gly Met Ile 250 931 atc att ggt ggc gga ctg tcc aat gct gcc gac ctt tat ttg gat cgc Ile Ile Gly Gly Leu Ser Asn Ala Ala Asp Leu Tyr Leu Asp Arg 265 teg gte aac cac tat tee ace ege ate gte gge gea gga tat ege eet 979 Ser Val Asn His Tyr Ser Thr Arg Ile Val Gly Ala Gly Tyr Arg Pro 280 285 ttg gca cgc gtt gcc aca gct cag ttg ggt gcg gat gct ggc atg atc 1027 Leu Ala Arg Val Ala Thr Ala Gln Leu Gly Ala Asp Ala Gly Met Ile 1069 ggt gtc gct gat cta gct cga cgc tct gta gtg gaa gcc aac Gly Val Ala Asp Leu Ala Arg Arg Ser Val Val Glu Ala Asn 310 315 1092 taggtgtttt tcggtgggct gcg

<210> 24

<211> 323

<212> PRT

<213> Corynebacterium glutamicum

<400> 24

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Thr Asn Met Arg Ala Gly Leu Val Asp Glu Ser Gly Arg Ile Val Thr 20 25 30

Ser Leu Ser Ala Pro Ser Pro Arg Thr Thr Gln Ala Met Glu Gln Gly 35 40 45

Ile Phe Asp Leu Val Glu Gln Leu Lys Ala Glu Tyr Pro Val Gly Ala 50 55 60

Val Gly Leu Ala Val Ala Gly Phe Leu Asp Pro Glu Cys Glu Val Val 65 70 75 80

Arg Phe Ala Pro His Leu Pro Trp Arg Asp Glu Pro Val Arg Glu Lys

85 90 95 Leu Glu Asn Leu Leu Gly Leu Pro Val Arg Leu Glu His Asp Ala Asn 105 Ser Ala Ala Trp Gly Glu His Arg Phe Gly Ala Ala Gln Gly Ala Asp 115 120 Asn Trp Val Leu Leu Ala Leu Gly Thr Gly Ile Gly Ala Ala Leu Ile 135 Glu Lys Gly Glu Ile Tyr Arg Gly Ala Tyr Gly Thr Ala Pro Glu Phe 145 150 155 Gly His Leu Arg Val Val Arg Gly Gly Arg Ala Cys Ala Cys Gly Lys Glu Gly Cys Leu Glu Arg Tyr Cys Ser Gly Thr Ala Leu Val Tyr Thr Ala Arg Glu Leu Ala Ser His Gly Ser Phe Arg Asn Ser Gly Leu Phe 200 Asp Lys Ile Lys Ala Asp Pro Asn Ser Ile Asn Gly Lys Thr Ile Thr 215 Ala Ala Arg Gln Glu Asp Pro Leu Ala Leu Ala Val Leu Glu Asp Phe Ser Glu Trp Leu Gly Glu Thr Leu Ala Ile Ile Ala Asp Val Leu Asp Pro Gly Met Ile Ile Gly Gly Gly Leu Ser Asn Ala Ala Asp Leu Tyr Leu Asp Arg Ser Val Asn His Tyr Ser Thr Arg Ile Val Gly Ala Gly Tyr Arg Pro Leu Ala Arg Val Ala Thr Ala Gln Leu Gly Ala 295 Asp Ala Gly Met Ile Gly Val Ala Asp Leu Ala Arg Arg Ser Val Val 310 315 Glu Ala Asn

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<211> 1785

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<222> (101)..(1762)

<223> RXA01814

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gcc ggg caa ctc o	-	-		
gtc acc gca tat t Val Thr Ala Tyr I 25				
cag gtc gct ttc g Gln Val Ala Phe (40				_
gct ttc aac gag o Ala Phe Asn Glu A 55				
tac cgc aac cag o Tyr Arg Asn Gln (70	-			
cgc gat acg cac of Arg Asp Thr His A				
gtc ctc att gcc a Val Leu Ile Ala A 105				
tac acc ccg acg of Tyr Thr Pro Thr I 120		His Ala Ile	_	
ggc atc atc ctt of Gly Ile Ile Leu (135				
atc gtg atc acc of the Val Ile Thr I				
tac aac cca gcc a Tyr Asn Pro Ala A			-	
atc gcc aac cgc q Ile Ala Asn Arg A 185				
aag cga gtt cca q Lys Arg Val Pro V 200				
gac ttc aag ggc a Asp Phe Lys Gly 1 215				
gat gcc atc cgc g	gaa gct ggt gtt	cga atc ggc	gca gac cca	atg ggt 835

Asp 230	Ala	Ile	Arg	Glu	Ala 235	Gly	Val	Arg	Ile	Gly 240	Ala	Asp	Pro	Met	Gly 245	
	_			_		tgg Trp		-		_	_					883
						cca Pro										931
						aag Lys										979
-	_	_	_	_		gac Asp 300		_	_	_				_		1027
		-	_	_	_	gac Asp	_				-			-	_	1075
	_	_				cac His			_	_	-					1123
	-		_			tgg Trp		_	_		_					1171
_	_	_			_	atc Ile	_	_	_			_			_	1219
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			_			ttc Phe			_	-		_		_		1315
						acc Thr										1363
						gct Ala										1411
						gaa Glu										1459
	-	_		_	_	gaa Glu 460	_		_	-		_	_		-	1507
_	_	_			-	cag Gln	_		_		-		-		_	1555

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	acc acc gaa aac gcc Thr Thr Glu Asn Ala 510		
	aag tac aag atc tac Lys Tyr Lys Ile Tyr 525	-	
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Phe Ala Leu Asp Ser 50	Ala Phe Asn Glu Asp 55	His Ile Leu Ala Thr 60	Thr
Gln Ala Ile Val Asp 65	Tyr Arg Asn Gln Gln 70	Pro Lys Asn Trp Val 75	Gly 80
Pro Leu Phe Ile Gly 85	Arg Asp Thr His Ala 90	Leu Ser Glu Pro Ala 95	Met
Ile Ser Ala Leu Glu 100	Val Leu Ile Ala Asn 105	Asp Val Glu Val Leu 110	Val
Asp Ala Asp Gly Arg 115	Tyr Thr Pro Thr Pro 120	Ala Val Ser His Ala 125	Ile
Leu Arg His Asn Asp 130	Gly Ile Ile Leu Gly 135	Thr Ala Gly Pro Ser 140	Arg
Pro Tyr Ala Asp Gly 145	Ile Val Ile Thr Pro 150	Ser His Asn Pro Pro 155	Arg 160
Asp Gly Gly Phe Lys 165	Tyr Asn Pro Ala Asn 170	Gly Gly Pro Ala Asp 175	Thr

Asp Ala Thr Asp Trp Ile Ala Asn Arg Ala Asn Asp Ile Leu Arg Gly 180 185 Asp Leu Ala Asp Val Lys Arg Val Pro Val Ser Gly Val Leu Asp Glu 200 Arg Thr Thr Ala Tyr Asp Phe Lys Gly Ile Tyr Ile Ala Asp Leu Pro 215 Asn Val Val Asn Ile Asp Ala Ile Arg Glu Ala Gly Val Arg Ile Gly Ala Asp Pro Met Gly Gly Ala Ser Val Asp Tyr Trp Gly Ala Ile Ala Glu Thr His Gly Leu Asn Leu Thr Val Val Asn Pro His Val Asp Ser 265 Thr Phe Arg Phe Met Thr Leu Asp Thr Asp Gly Lys Ile Arg Met Asp Cys Ser Ser Pro His Ala Met Ala Ser Leu Ile Asp Asn Arg Asp Lys 295 Phe Asp Val Ala Thr Gly Asn Asp Ala Asp Ala Asp Arg His Gly Ile Val Thr Pro Asp Ala Gly Leu Met Asn Pro Asn His Tyr Leu Ala Val 325 330 Ala Ile Glu Tyr Leu Phe Ala His Arg Pro Gly Trp Ser Ala Asp Thr Ala Val Gly Lys Thr Leu Val Ser Ser Ser Met Ile Asp Arg Val Val Ala Gln Leu Gly Arg Thr Leu Val Glu Val Pro Val Gly Phe Lys Trp 375 Phe Val Pro Gly Leu Ile Ser Gly Glu Ile Gly Phe Gly Gly Glu Glu Ser Ala Gly Ala Ser Phe Leu Arg Met Asp Gly Thr Thr Trp Ser Thr Asp Lys Asp Gly Leu Ile Leu Asp Leu Leu Ala Ala Glu Ile Ile Ala 425 Val Thr Gly Lys Thr Pro Ser Gln Arg Tyr Ala Glu Leu Ala Glu Glu 440 Phe Gly Ala Pro Ala Tyr Ala Arg Thr Asp Ala Glu Ala Asn Arg Glu 450 455 Gln Lys Ala Ile Leu Lys Ala Leu Ser Pro Glu Gln Val Thr Ala Thr 470 475 Glu Leu Ala Gly Glu Ala Ile Thr Ala Lys Leu Thr Glu Ala Pro Gly

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485

Asn Gly Ala Ala Ile Gly Gly Leu Lys Val Thr Thr Glu Asn Ala Trp 500 505 510

Phe Ala Ala Arg Pro Ser Gly Thr Glu Asp Lys Tyr Lys Ile Tyr Ala 515 520 525

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Gln Ala Leu Val Ser Glu Val Leu Gly Gln 545 550

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<222> (1)..(657)

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gca ttc ctc acc gat gat tat ggc gct gac atg ggc gtg atg att tct 144 Ala Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser 35 40 45

gca tcc cac aac cca atg ccg gac aac gga atc aag ttc ttt tct gca 192
Ala Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala
50 55 60

ggt gga cac aag ctt cca gac cat gtg gaa gac gag att gag cgt gtt 240 Gly Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val
65 70 75 80

atg gac agc ttg cca gca gaa ggc cca aca ggg cat gga gtt ggc cgt 288 Met Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg

gtc atc gaa gaa gca acc gat gca cag gac cgt tac cta gag cac ctg 336 Val Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu 100 105 110

aag gaa gct gtt cct acg tca ctt gaa ggc atc aag att gtt gtg gat 384 Lys Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp

gca gcc aat ggt gcg gca agt gtt gta gct cca acg gct tat gag gct Ala Ala Asn Gly Ala Ala Ser Val Val Ala Pro Thr Ala Tyr Glu Ala 130 135 140

gcg ggt gca act gta att gct att cat aac aag cca gac tca tac aac 480

528

576

624

680

Ala Gly Ala Thr Val Ile Ala Ile His Asn Lys Pro Asp Ser Tyr Asn 150 155 atc aac atg gac tgc ggt tcc acc cac att gat cag gcg cag ccg cca Ile Asn Met Asp Cys Gly Ser Thr His Ile Asp Gln Ala Gln Pro Pro 165 170 gtc ttg aag cac ggt gct gac ctt gga ctc gcg cat gac ggt gat gct Val Leu Lys His Gly Ala Asp Leu Gly Leu Ala His Asp Gly Asp Ala 185 gac cgt tgt ttg gct gtg aac aag gat gcc aac ctt gtt gat ggt gac Asp Arg Cys Leu Ala Val Asn Lys Asp Ala Asn Leu Val Asp Gly Asp 200 caa atc atg gcg ctg tta gcc att gcg atg aaa taaaacggcg agctgcgcaa 677 Gln Ile Met Ala Leu Leu Ala Ile Ala Met Lys 210 215 gaa <210> 28 <211> 219 <212> PRT <213> Corynebacterium glutamicum <400> 28 Val Ser Gly Glu Met Leu Ala Ala Ala Leu Ser Ala Gly Met Ala Ser Gln Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val Ala Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser Ala Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp Ala Ala Asn Gly Ala Ala Ser Val Val Ala Pro Thr Ala Tyr Glu Ala 130 135 Ala Gly Ala Thr Val Ile Ala Ile His Asn Lys Pro Asp Ser Tyr Asn 150 155 Ile Asn Met Asp Cys Gly Ser Thr His Ile Asp Gln Ala Gln Pro Pro 165 170

Val Leu Lys His Gly Ala Asp Leu Gly Leu Ala His Asp Gly Asp Ala 180 185 Asp Arg Cys Leu Ala Val Asn Lys Asp Ala Asn Leu Val Asp Gly Asp 195 200 Gln Ile Met Ala Leu Leu Ala Ile Ala Met Lys 215 <210> 29 <211> 399 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(399) <223> FRXA02803 <400> 29 tct gga gag atg ctc gcg gca gca ctt tca gca ggc atg gcc agc cag 48 Ser Gly Glu Met Leu Ala Ala Ala Leu Ser Ala Gly Met Ala Ser Gln ggt gtt gat gtc att cgt gtt ggt gtc atc cca acc cca gct gtt gca 96 Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val Ala tto oto acc gat gat tat ggo got gao atg ggo gtg atg att tot goa 144 Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser Ala 35 tcc cac aac cca atg ccg gac aac gga atc aag ttc ttt tct gca ggt 192 Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly gga cac aag ctt cca gac cat gtg gaa gac gag att gag cgt gtt atg 240 Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met 65 gac agc ttg cca gca gaa ggc cca aca ggg cat gga gtt ggc cgt gtc 288 Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val atc gaa gaa gca acc gat gca cag gac cgc tac cta gag cac ctg aag 336 Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys 100 gaa gct gtt cct acg tca ctt gaa ggc atc aag att gtt gtg gat gca 384 Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp Ala 115 120 399 gcc aat ggt gcg gca Ala Asn Gly Ala Ala 130

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Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser Ala 35 40 45

Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly 50 55 60

Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met 65 70 75 80

Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val 85 90 95

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Met Asp Glu Ser Arg

1

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cgc cat cag atg aat gtt ttg cag gta acc aga act aca gca ggt gtt 211 Arg His Gln Met Asn Val Leu Gln Val Thr Arg Thr Thr Ala Gly Val 25 30 35

gct agt tgg ttg gca gaa cgt gcg gca cta aat cca gtg ccg cat ttg 259 Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn Pro Val Pro His Leu 40 45 50

gtt cct gag gat gaa aca gga atc ggc agg gcg ttg tat ccc caa gat 307

Val	Pro 55	Glu	Asp	Glu	Thr	Gly 60	Ile	Gly	Arg	Ala	Leu 65	Tyr	Pro	Gln	Asp	
							ggg Gly									355
							gag Glu									403
	-	_			_		agc Ser		_	_	_		_		-	451
		_			_	_	gcg Ala 125		-	_		_	-	_		499
				-			tac Tyr	_			-				_	547
							cct Pro									595
							cct Pro									643
							gat Asp									691
							gtg Val 205									739
						His	ggt Gly	Val	Gly	Gly						787
							ccc Pro									835
							ccc Pro									883
						_	ttg Leu	_	_	_	_	_	_	_		931
-	-		_				gat Asp 285			_	_	_	_	-		979
		-		-	-		ggc Gly		_	_				-		1027

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					gct Ala 315											1075
		_			gtt Val	_		_				_	_		_	1123
			_		gat Asp				_					_	_	1171
				_	tcg Ser		-	_	_			-		_		1219
_		-			gaa Glu	_				_	_	_		-	_	1267
	_	-	_	-	ggc Gly 395					-		_				1315
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					tat Tyr											1411
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_		-			gga Gly			_							_	1507
					ttg Leu 475											1555
					tct Ser											1603
	-		_	-	agc Ser			_	-	-		-	_	_		1651
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<400> 32

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Thr Thr Ala Gly Val Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn 35 40 45

Pro Val Pro His Leu Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala 50 55 60

Leu Tyr Pro Gln Asp Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala 65 70 75 80

Arg Tyr Gly Ser His Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala 85 90 95

Gly Ala Gly Phe Glu Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro 100 105 110

Leu Ile Pro Trp Leu Val Asn Lys His Gly Leu Asp Ala Gly Val Gln
115 120 125

Ile Thr Ala Ser His Asn Gly Ala Ala Asp Asn Gly Tyr Lys Val Phe 130 135 140

Leu Ser Asn Gly Arg Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu 145 150 155 160

Ala His Ile Asn Ala Val Glu Asp Pro Ile Arg Val Pro Arg Val Thr
165 170 175

Val Arg Pro Thr Ala Asp Gln Leu Arg Arg Tyr Val Asp Glu Met Val 180 185 190

Ser Leu Val Thr Pro Asp Gln Ala Asp Leu Leu Arg Val Asn Ser Glu 195 200 205

Arg Gly Asn Leu Arg Val Val Tyr Thr Ala Leu His Gly Val Gly 210 215 220

Arg Ala Met Ala Asn Ala Phe Gln Phe Ala Gly Phe Pro His Thr His 225 230 235 240

Gly Val Lys Ala Gln Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala 245 250 255

Phe Pro Asn Pro Glu Glu Pro Ser Ala Ile Glu Leu Leu Glu Arg
260 265 270

Ala Lys Glu Lys Asn Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala 275 280 285

Asp Arg Cys Ala Val Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met

290 295 300 Leu Ser Gly Asp Glu Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro 310 315 Glu Tyr Ser Gly Glu Gly Pro Arg Pro Val Val Ala Thr Thr Val Val 325 330 Ser Ser Gln Leu Leu Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr 345 Ser Glu Thr Leu Thr Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly 355 360 Leu Asp Gly Pro Leu Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys Pro Val Pro Asp Val Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu 385 395 Phe Met Ala Ser Trp Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu Gln Gln Lys Leu Asn Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser Ser Gln Ile Ala Val Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His Trp Ile Ala His Pro Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro 455 His Ile Leu Pro Glu Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly 470 475 His Val His Ile Arg Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys 490 Ala Lys Leu Tyr Leu Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala 505 Ala Gln Leu His Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser 520 Lys Leu 530 <210> 33 <211> 1684 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1684) <223> FRXA02854 <400> 33

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cag ctt agt ttc (Gln Leu Ser Phe (, , , , ,	,,,		, , ,
cgc cat cag atg a Arg His Gln Met A 25				
gct agt tgg ttg (Ala Ser Trp Leu A				
gtt cct gag gat (Val Pro Glu Asp (55				
ggt ccg ttg cgg of Gly Pro Leu Arg v			Arg Tyr Gly	
act ttt gct gca a Thr Phe Ala Ala :				
gtg acg ttg ctc o Val Thr Leu Leu l 105	_			
gtg aac aag cat o Val Asn Lys His (120	Sly Leu Asp A			
aat ggt gcg gcg g Asn Gly Ala Ala A 135				
cag ctt tat tct of Gln Leu Tyr Ser (150			Ala His Ile	
gtg gaa gat ccg a Val Glu Asp Pro I				
gat cag ctg cgt o Asp Gln Leu Arg <i>l</i> 185				
gat cag gct gat t Asp Gln Ala Asp 1 200	Leu Leu Arg V			
gtg gtg tat acc g Val Val Tyr Thr A 215				
gct ttc caa ttt (gct ggt ttt d	ccc cat act cat	ggc gtg aag	gct cag 835

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				att Ile												931
_	_		_	ttt Phe			_		_	-	_	_	_	_		979
		_		gct Ala	-				_	_				_		1027
				ttg Leu												1075
				gtg Val 330												1123
			_	gag Glu	-				_			-		_	_	1171
				ctg Leu	_		_	_	_			-		_		1219
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Ala gtg Val 390 gct Ala	Phe 375 ccg Pro gcc Ala	Ala gat Asp gaa Glu tat	Tyr aag Lys ctg Leu cgc	gac Asp aag Lys	Glu ggc Gly 395 gct Ala	Ala 380 atc Ile cag Gln	tct ser ggc Gly	Gly aca Thr gca Ala	Thr gcg Ala agc Ser 415 gcg	ttg Leu 400 ctg Leu	Pro 385 ttc Phe cag Gln	Val atg Met caa Gln caa	Pro gcg Ala aaa Lys	Asp tcg Ser ctc Leu 420 gct	tgg Trp 405 aat Asn	1315
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gtg Val 390 gct Ala gag Glu cgc Arg	Phe 375 ccg Pro gcc Ala ttg Leu acg Thr	Ala gat Asp gaa Glu tat Tyr agc Ser 440 gaa	Tyr aag Lys ctg Leu cgc Arg 425 agt Ser	gac Asp aag Lys 410 cga Arg	ggc Gly 395 gct Ala tat Tyr cgc Arg	Ala 380 atc Ile cag Gln ggg Gly gag Glu gtg	tct Ser ggc Gly tat Tyr tta Leu 445	Gly aca Thr gca Ala ttt Phe 430 gtt Val	Thr gcg Ala agc Ser 415 gcg Ala gat Asp	Cys ttg Leu 400 ctg Leu tcc Ser cac His	Pro 385 ttc Phe cag Gln tcg Ser tgg Trp	Val atg Met caa Gln caa Gln att Ile 450 att	gcg Ala aaa Lys att Ile 435 gcg Ala	Asp tcg Ser ctc Leu 420 gct Ala cat His	tgg Trp 405 aat Asn gtg Val cct Pro	1315 1363 1411

1603

1651

1684

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220

210 215 Arg Ala Met Ala Asn Ala Phe Gln Phe Ala Gly Phe Pro His Thr His 230 235 Gly Val Lys Ala Gln Gln Tyr Pro Asp Pro Thr Phe Pro Thr Val Ala 245 250 Phe Pro Asn Pro Glu Glu Pro Ser Ala Ile Glu Leu Leu Glu Arg 265 Ala Lys Glu Lys Asn Ala Asp Ile Leu Phe Ala Leu Asp Pro Asp Ala Asp Arg Cys Ala Val Gly Ile Arg Thr Ala Asp Gly Gly His Arg Met Leu Ser Gly Asp Glu Val Gly Thr Leu Leu Ala Thr Arg Leu Val Pro 305 315 Glu Tyr Ser Gly Glu Gly Pro Arg Pro Val Val Ala Thr Thr Val Val Ser Ser Gln Leu Leu Gly Ile Ile Ala Glu Asp Lys Gly Trp Asp Tyr Ser Glu Thr Leu Thr Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly 360 Leu Asp Gly Pro Leu Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys 375 Pro Val Pro Asp Val Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu 395 Phe Met Ala Ser Trp Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu Gln Gln Lys Leu Asn Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser Ser Gln Ile Ala Val Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His Trp Ile Ala His Pro Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro His Ile Leu Pro Glu Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly His Val His Ile Arg Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys 485 Ala Lys Leu Tyr Leu Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala 505 Ala Gln Leu Leu His Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser 515 520 525

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ttg aag att gct atg gat gaa gcc gga att aca ctg cgt acc acc aag
                                                                    96
Leu Lys Ile Ala Met Asp Glu Ala Gly Ile Thr Leu Arg Thr Thr Lys
gta gga gac cgc tac gtg ctg gaa gac ctc aat gca ggt gga ttc agc
                                                                    144
Val Gly Asp Arg Tyr Val Leu Glu Asp Leu Asn Ala Gly Gly Phe Ser
                             40
                                                                    192
ctg ggc ggc gag caa tct ggc cac att gtt ctt cca gat cat ggc acc
Leu Gly Gly Glu Gln Ser Gly His Ile Val Leu Pro Asp His Gly Thr
                         55
act ggc gat gga act ttg act ggt ctt tcc atc atg gcg cgc atg gct
                                                                    240
Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala
 65
                     70
                                          75
gaa acc gga aag tcc ttg ggc gag ttg gca caa gct atg acg gtg ctg
                                                                    288
Glu Thr Gly Lys Ser Leu Gly Glu Leu Ala Gln Ala Met Thr Val Leu
                 85
cca cag gtt ctg atc aat gtg cca gtt tcg gat aag tcc acc atc gtg
                                                                    336
Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val
            100
                                 105
age cae cea age gtt gtg get geg ate geg gaa gea gaa get gag ttg
                                                                    384
Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu
        115
gge gee ace ggt ege gtt ett ett egt get tet gge ace gaa qaq ett
                                                                    432
Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu
                        135
    130
tte ege gtg atg gtt gag get gga gae aag gaa eaa get egt egt ate
                                                                    480
Phe Arg Val Met Val Glu Ala Gly Asp Lys Glu Gln Ala Arg Arg Ile
145
                    150
                                         155
                                                             160
gcg gga cgt ctt .gct gca gtg gtt gca gaa gtc taattcactt cagtcacagc 533
Ala Gly Arg Leu Ala Ala Val Val Ala Glu Val
                165
                                     170
                                                                    536
gca
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<212> PRT

<213> Corynebacterium glutamicum

<400> 36

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Leu Lys Ile Ala Met Asp Glu Ala Gly Ile Thr Leu Arg Thr Thr Lys
20 25 30

Val Gly Asp Arg Tyr Val Leu Glu Asp Leu Asn Ala Gly Gly Phe Ser 35 40 45

Leu Gly Gly Glu Gln Ser Gly His Ile Val Leu Pro Asp His Gly Thr 50 55 60

Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala 65 70 75 80

Glu Thr Gly Lys Ser Leu Gly Glu Leu Ala Gln Ala Met Thr Val Leu 85 90 95

Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val 100 105 110

Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu 115 120 125

Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu 130 135 140

Phe Arg Val Met Val Glu Ala Gly Asp Lys Glu Gln Ala Arg Arg Ile 145 150 155 160

Ala Gly Arg Leu Ala Ala Val Val Ala Glu Val
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<210> 37

<211> 1497

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1474)

<223> RXN01365

<400> 37

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ttgcaagcgt tattttgttc cctaacccct tcgaggattt atg cgt acc cgt gaa 115
Met Arg Thr Arg Glu
1 5

tct gtc aca gct gta att aag gcg tat gac gtc cgt ggt gtt gtt ggt $\,$ 163 Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly $\,$ 10 $\,$ 15 $\,$ 20

gtc gat att gat gct gat ttc att tct gag act ggc gct gcc ttt ggt 211

Val	Asp	Ile	Asp 25	Ala	Asp	Phe	Ile	Ser 30	Glu	Thr	Gly	Ala	Ala 35	Phe	Gly	
							gaa Glu 45									259
							ttg Leu					_	-			307
							gtt Val									355
-	-						acc Thr	_	_	_	_			_		403
							gag Glu									451
							cag Gln 125									499
							cca Pro								_	547
-			_	_	_	_	agc Ser	_		-						595
			_	_			cgc Arg	_	_	_	_	-		-		643
							act Thr									691
							tat Tyr 205									739
			-			_	gag Glu		_		_	_	-	_	_	787 ·
_			_				tct Ser	_			-			-		835
							gtc Val									883
							gta Val									931

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265		270	:	275	
ccg ggt tcc acc Pro Gly Ser Thr 280	Ile Ile His A				979
gag gtg att gct Glu Val Ile Ala 295					1027
cac tcc ttc atc His Ser Phe Ile 310		Met Ala Glu			1075
ggc gag cac tct Gly Glu His Ser					1123
tcc ggc att ttg Ser Gly Ile Leu 345			Ala Ala Leu (1171
gac cag cca ctc Asp Gln Pro Leu 360	Ser Glu Met M				1219
tca ggc gag ttg Ser Gly Glu Leu 375					1267
cgc acc cag gct Arg Thr Gln Ala 390		Ala Phe Ala	-		1315
gac acc ctt gac Asp Thr Leu Asp					1363
ttc aac gtg cgt Phe Asn Val Arg 425			Leu Leu Arg 1		1411
gaa gct gca tcg Glu Ala Ala Ser 440	Lys Glu Glu V				1459
ggg att atc cgc Gly Ile Ile Arg 455	•	t ttccggcgg	g cat		1497
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Arg Gly Val Val	Gly Val Asp I	Ile Asp Ala	Asp Phe Ile S	Ser Glu Thr	

20 25 30 Gly Ala Ala Phe Gly Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val His Leu Gly Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys 85 Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp 135 Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala 145 Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys 165 Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn 215 Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly 230 Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg Tyr Leu Glu Lys Leu Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr Ser Lys Ala Val Pro Glu Val Ile Ala Glu Asn Gly Gly Thr Ala Val 295 Arg Thr Arg Val Gly His Ser Phe Ile Lys Ala Lys Met Ala Glu Thr 310 315 Gly Ala Ala Phe Gly Gly Glu His Ser Ala His Tyr Tyr Phe Thr Glu 325 Phe Phe Asn Ala Asp Ser Gly Ile Leu Ala Ala Met His Val Leu Ala 340 345

Ala Leu Gly Ser Gln Asp Gln Pro Leu Ser Glu Met Met Ala Arg Tyr 355 360 Asn Arg Tyr Val Ala Ser Gly Glu Leu Asn Ser Arg Leu Ala Asn Ala 375 Glu Ala Gln Glu Arg Thr Gln Ala Val Leu Asp Ala Phe Ala Asp 385 390 395 Arg Thr Glu Ser Val Asp Thr Leu Asp Gly Val Thr Val Glu Leu Lys Asp Thr Ser Ala Trp Phe Asn Val Arg Ala Ser Asn Thr Glu Pro Leu 425 Leu Arg Leu Asn Val Glu Ala Ala Ser Lys Glu Glu Val Asp Ala Leu Val Ala Glu Ile Leu Gly Ile Ile Arg Ala 455 <210> 39 <211> 994 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(994) <223> FRXA01365 <400> 39 cctgatcagg acgaatcata aggtttgcta ttcggattgg atcctttggc aggggtagga 60 ttgcaagcgt tattttgttc cctaacccct tcgaggattt atg cgt acc cgt gaa 115 Met Arg Thr Arg Glu 1 tct gtc aca gct gta att aag gcg tat gac gtc cgt ggt gtt gtt ggt 163 Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly gte gat att gat get gat tte att tet gag act gge get gee ttt ggt 211 Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly cgg ctc atg cgt agt gag ggt gaa acc acc gtt gct att ggc cat gac 259 Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val Ala Ile Gly His Asp 45 atg cgt gat tee tee eet gaa ttg gee aag geg ttt gee gat gge gtg 307 Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala Phe Ala Asp Gly Val 60 act gca cag ggt ttg gat gtt gtt cat ttg gga ctg act tct act gat 355 Thr Ala Gln Gly Leu Asp Val Val His Leu Gly Leu Thr Ser Thr Asp 80

gag ctg tac ttt gcg tcc gga acc ttg aag tgt gct ggt gcg atg ttt

403

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Glu	Leu	Tyr	Phe	Ala 90	Ser	Gly	Thr	Leu	Lys 95	Cys	Ala	Gly	Ala	Met 100	Phe	
				aac Asn												451
				ccg Pro												499
				gag Glu												547
				gat Asp												595
		-	-	aag Lys 170				_	_	_	_	_		_		643
_			_	ggt Gly				_			_		_		_	691
		-	_	gcg Ala		_					-					739
				aat Asn		-	_		_		_	_	_	_	_	787
				gag Glu												835
_		-	-	tgc Cys 250			_	_		_		_		_	_	883
				tgt Cys												931
_				atc Ile				_				_	_			979
	gtg Val 295		_	_												994

<210> 40 <211> 298 <212> PRT

<213> Corynebacterium glutamicum

<400> 40

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Arg Gly Val Val Gly Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr 20 25 30

Gly Ala Ala Phe Gly Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val\$35\$ 40 45

Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala 50 55 60

Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly 65 70 75 80

Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys $85 \hspace{1cm} 90 \hspace{1cm} 95$

Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly 100 105 110

Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly 115 120 125

Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp 130 135 . 140

Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala 145 150 155 160

Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys 165 170 175

Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu 180 185 190

Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu 195 200 205

Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn 210 220

Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly 225 230 235 240

Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys 245 250 255

Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg 260 265 270

Tyr Leu Glu Lys Leu Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr 275 280 285

Ser Lys Ala Val Pro Glu Val Ile Ala Glu 290 295

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gac cca gca gac ctc gtt tct gtg ttg gaa gac ctc gat gca gaa tcc

Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp Leu Asp Ala Glu Ser

691

	185	•			190				195			
-	ttc gtg Phe Val 200	_	_					-		_	_	739
	gct cgt Ala Arg		-	-		_		 _				787
	gtc gcg Val Ala	_	s Phe	_	-				-	_	_	835
	gag tto Glu Phe		_	_	_		_				-	883
	gga ggt Gly Gly 265	Arg Ty										931
	gtg ato Val Ile 280		-	-		_	_					979
	atg gat Met Asp	-		-			_	_	_		-	1027
	ttg atg Leu Met		ı Leu									1075
	acc cac Thr His											1123
	tac ctc Tyr Leu 345	Gln Gl	-		_	_			_		-	1171
	gac ggc Asp Gly 360											1219
	cct ggc Pro Gly											1267
	act cgc Thr Arg		l Pro									1315
	gat ctt Asp Leu											1363
	ttc ttc Phe Phe 425	Ala Gl										1411

_	gag Glu		_		_	 -	_			_	_		_	1459
	atg Met 455													1507
	cct Pro					 _		_	_		_			1555
_	gtt Val	_				 _					-		 	1603
	gaa Glu													1651
	gaa Glu													1699
-	tgg Trp 535		_	_		 tagt	ceget	tg (cttat	agg	gt ca	ag		1743
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<212> PRT

<213> Corynebacterium glutamicum

<400> 42

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Tyr Ser Asn Phe Gln Ala Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu 20 25 30

Asn Arg Ala Glu Lys Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp $35 \hspace{1cm} 40 \hspace{1cm} 45$

Leu Ser Lys Asn Leu Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala 50 55 60

Leu Thr Glu Glu Ser Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala 65 70 75 80

Gly Glu His Leu Asn Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala 85 90 95

Leu Arg Leu Pro Ala Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val 100 105 110

Ala Ala Asp Val His Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr 115 120 125

Ala Leu Arg Ser Gly Asn Trp Leu Gly His Thr Gly His Thr Ile Lys

130 135 140 Lys Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala Met 150 155 Ala Thr Lys Ala Leu Arg Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu 165 Phe Val Ser Asn Val Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp 185 Leu Asp Ala Glu Ser Thr Leu Phe Val Ile Ala Ser Lys Thr Phe Thr Thr Gln Glu Thr Leu Ser Asn Ala Arg Ala Ala Arg Ala Trp Leu Val 215 Glu Lys Leu Gly Glu Glu Ala Val Ala Lys His Phe Val Ala Val Ser Thr Asn Ala Glu Lys Val Ala Glu Phe Gly Ile Asp Thr Asp Asn Met Phe Gly Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser Val Asp Ser Ala Val Gly Leu Ser Leu Met Ala Val Ile Gly Pro Arg Asp Phe Met Arg Phe Leu Gly Gly Phe His Ala Met Asp Glu His Phe Arg Thr Thr Lys Phe Glu Glu Asn Val Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr 315 Ser Asp Phe Tyr Gly Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu Asp Leu Ser Arg Phe Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser Asn Gly Lys Ser Val His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr Gly Glu Ile Tyr Trp Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe 375 Phe Gln Leu Ile His Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile 390 395 Gly Phe Ala Arg Pro Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met 410 405 His Asp Leu Leu Met Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala 425 Phe Gly Lys Asn Ala Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu 435 Leu Val Asn His Lys Val Met Pro Gly Asn Arg Pro Thr Thr Ile 455

Leu Ala Glu Glu Leu Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu 465 470 475 Tyr Glu His Ile Val Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu 500 505 Ala Pro Ala Val Ser Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser Thr Asp Ser Leu Ile Lys Trp Tyr Arg Ala Asn Arg 530 535 <210> 43 <211> 630 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(630) <223> RXA01989 <400> 43 gtt aaa tca att cac aaa aca att cat gaa ggt act ggt gca ggt agt 48 Val Lys Ser Ile His Lys Thr Ile His Glu Gly Thr Gly Ala Gly Ser gac ttc tta ggc tgg gtt gat tta cca gtt gat tac gac aaa gaa gaa 96 Asp Phe Leu Gly Trp Val Asp Leu Pro Val Asp Tyr Asp Lys Glu Glu 20 ttt tca aga att gtt gaa gca tca aaa cgc att aaa gaa aat tct gat 144 Phe Ser Arg Ile Val Glu Ala Ser Lys Arg Ile Lys Glu Asn Ser Asp 35 gtt tta gta gtc atc ggt att ggt ggt tct tac tta ggt gca cgt gca 192 Val Leu Val Val Ile Gly Ile Gly Gly Ser Tyr Leu Gly Ala Arg Ala gca atc gaa atg tta acg tca tca ttt aga aac agc aat gaa tac cct 240 Ala Ile Glu Met Leu Thr Ser Ser Phe Arg Asn Ser Asn Glu Tyr Pro gaa att gta ttt gtt ggt aat cac tta tca tca aca tat acg aaa gag 288 Glu Ile Val Phe Val Gly Asn His Leu Ser Ser Thr Tyr Thr Lys Glu tta gtt gat tat tta gca gac aaa gat ttc tct gta aac gtt att tct 336 Leu Val Asp Tyr Leu Ala Asp Lys Asp Phe Ser Val Asn Val Ile Ser 100 105 aaa tot ggt aca act aca gaa coa gca gtt gca ttt aga ttg tto aaa 384 Lys Ser Gly Thr Thr Glu Pro Ala Val Ala Phe Arg Leu Phe Lys 120

caa tta gtt gaa gaa aga tac ggt aaa gaa gaa gca caa aaa cgt ata

432

Gln Leu Val Glu 130	Glu Arg	Tyr Gly 135	Lys G	Slu Glu	Ala Gln 140	Lys .	Arg	Ile	
ttt gca aca acg Phe Ala Thr Thr 145	, -	Glu Lys			_	_	_		480
aac gaa ggt tat Asn Glu Gly Tyn			Val P	_		Gly		_	528
tat tct gtt tta Tyr Ser Val Let 180	Thr Ala				_		-		576
att aac atc gaa Ile Asn Ile Glu 195		_	Gly A	_	-	_	-	-	624
tta tct Leu Ser 210									630
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Phe Ser Arg Ile	Val Glu	Ala Ser	Lys A	rg Ile	Lys Glu	Asn	Ser	Asp	
		40			45				
Val Leu Val Val 50	Ile Gly			Ser Tyr	45	Ala	Arg	Ala	
		Ile Gly 55 Ser Ser	Gly S		45 Leu Gly 60		-		
50 Ala Ile Glu Met	Leu Thr	Ile Gly 55 Ser Ser	Gly S Phe A Leu S	arg Asn 75	45 Leu Gly 60 Ser Asn	Glu '	Tyr	Pro 80	
50 Ala Ile Glu Met 65	Leu Thr 70 Val Gly 85 Leu Ala	Ile Gly 55 Ser Ser	Gly S Phe A Leu S	arg Asn 75 Ser Ser 90	45 Leu Gly 60 Ser Asn Thr Tyr	Glu f	Tyr Lys 95	Pro 80 Glu	
50 Ala Ile Glu Met 65 Glu Ile Val Phe	Leu Thr 70 Val Gly 85 Leu Ala	Ile Gly 55 Ser Ser Asn His	Gly S Phe A Leu S Asp P 105 Ala V	arg Asn 75 Ser Ser 90 Phe Ser	Leu Gly 60 Ser Asn Thr Tyr Val Asn	Glu Thr Thr Val 110	Tyr Lys 95 Ile	Pro 80 Glu Ser	
50 Ala Ile Glu Met 65 Glu Ile Val Phe Leu Val Asp Tyr 100 Lys Ser Gly Thr	Leu Thr 70 Val Gly 85 Leu Ala	Ser Ser Asn His Asp Lys Glu Pro	Gly S Phe A Leu S Asp P 105 Ala V	arg Asn 75 Ser Ser 90 Phe Ser	45 Leu Gly 60 Ser Asn Thr Tyr Val Asn Phe Arg 125	Thr :	Tyr Lys 95 Ile Phe	Pro 80 Glu Ser Lys	
Ala Ile Glu Met 65 Glu Ile Val Phe Leu Val Asp Tyr 100 Lys Ser Gly Thr 115 Gln Leu Val Glu	Leu Thr 70 Val Gly 85 Leu Ala Thr Thr	Ile Gly 55 Ser Ser Asn His Asp Lys Glu Pro 120 Tyr Gly 135 Glu Lys	Gly S Phe A Leu S Asp P 105 Ala V Lys G	arg Asn 75 Ser Ser 90 Phe Ser Val Ala	45 Leu Gly 60 Ser Asn Thr Tyr Val Asn Phe Arg 125 Ala Gln 140	Glu f	Tyr Lys 95 Ile Phe Arg	Pro 80 Glu Ser Lys	

165 170 175 Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly 185 Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu 195 200 205 Leu Ser 210 <210> 45 <211> 1269 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1246) <223> RXA00340 <400> 45 cggtatctcc gacatccgca acacccccaa agatgaggtt ccacagtgcc cagaatgtgg 60 ctcttacctc atcactgaca tctcttagaa agaccaccca gtg aaa tta gtc atc 115 Val Lys Leu Val Ile gag gee gae gge tee ege gga aac eee gge gte gee gge tee gge 163 Glu Ala Asp Gly Gly Ser Arg Gly Asn Pro Gly Val Ala Gly Ser Gly 10 15 211 acc gtg gtg tac tcc gac aac aaa gca gaa gtt ctc aaa gaa atc gcc Thr Val Val Tyr Ser Asp Asn Lys Ala Glu Val Leu Lys Glu Ile Ala tat gtt gtc gga aca aaa gcc acc aac gtc gcc gaa tac cgc gga 259 Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val Ala Glu Tyr Arg Gly 4.5 307 cta etc gaa gge etc aaa gea gee ege gag etc gge get ace tee gtg Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu Gly Ala Thr Ser Val gat gtc tac atg gac tcc aaa ctt gtc gtt gaa caa atg tcc ggc cgg 355 Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu Gln Met Ser Gly Arg 75 tgg aaa atc aaa cac ccc gac atg aaa gtt cta gcg atc gaa gcc aag 403 Trp Lys Ile Lys His Pro Asp Met Lys Val Leu Ala Ile Glu Ala Lys 90 gag att gct tcc gaa atc ggg tcc gtt tct tat acg tgg att ccg cgt 451 Glu Ile Ala Ser Glu Ile Gly Ser Val Ser Tyr Thr Trp Ile Pro Arg 105 110 gag aaa aac aaa cga gct gac gca ttg tcc aac gtg gcg atg gat gct 499 Glu Lys Asn Lys Arg Ala Asp Ala Leu Ser Asn Val Ala Met Asp Ala 120 125

							ggt Gly									547
		_		-	-		ggc Gly				_	-			-	595
	-						tgg Trp			_			_			643
							ggc Gly									691
							cca Pro 205									739
							cga Arg									787
							acc Thr									835
							aaa Lys									883
							gat Asp									931
_		_		_	_		acc Thr 285	_				_			_	979
							ctg Leu									1027
							cgc Arg									1075
	-	_		_			atc Ile				_			_	-	1123
							cag Gln									1171
							gaa Glu 365									1219
ttc	aac	gac	acc	tca	cac	ctg	gaa	gcg	tgad	cgaca	agt o	ctgad	cggaa	ag		1266

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Phe Asn Asp Thr Ser His Leu Glu Ala 375 380

ctc 1269

<210> 46

<211> 382

<212> PRT

<213> Corynebacterium glutamicum

<400> 46

Val Lys Leu Val Ile Glu Ala Asp Gly Gly Ser Arg Gly Asn Pro Gly
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Val Ala Gly Ser Gly Thr Val Val Tyr Ser Asp Asn Lys Ala Glu Val 20 25 30

Leu Lys Glu Ile Ala Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val 35 40 45

Ala Glu Tyr Arg Gly Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu 50 55 60

Gly Ala Thr Ser Val Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu 65 70 75 80

Gln Met Ser Gly Arg Trp Lys Ile Lys His Pro Asp Met Lys Val Leu 85 90 95

Ala Ile Glu Ala Lys Glu Ile Ala Ser Glu Ile Gly Ser Val Ser Tyr 100 105 110

Thr Trp Ile Pro Arg Glu Lys Asn Lys Arg Ala Asp Ala Leu Ser Asn 115 120 125

Val Ala Met Asp Ala Ala Ala Gly Lys Pro Val Gly Val Val Gly 130 135 140

Asp Ser Ala Ser Val Ser Ser Ala Ser Ser Val Ala Gly Ser Glu Lys 145 150 155 160

Glu Asp Leu Asn Cys Thr Glu Thr Lys Pro Thr Asn Trp Asn Gly Ala 165 170 175

Thr Thr Asp Pro Thr Arg Phe Leu Leu Arg His Gly Gln Thr Ala 180 185 190

Met Ser Val Ala Arg Leu Tyr Ser Gly Arg Ser Asn Pro Glu Leu Ser 195 200 205

Glu Leu Gly Glu Lys Gln Ala Ala Ala Ala Ala Arg Arg Leu Ala Gln 210 215 220

Thr Gly Gly Ile Asp Ala Ile Val Ser Ser Pro Leu Thr Arg Thr Met 225 230 235 240

Gln Thr Ala Glu Ala Ala Ala Ala Leu Gly Met Lys Val Arg Val 245 250 255

Ile Asp Asp Leu Ile Glu Thr Asp Phe Gly Leu Trp Asp Gly Lys Ser

260 265 270 Phe Ser Glu Ala His Glu Gln Asp Pro Glu Leu His Thr Lys Trp Leu Thr Asp Ser Ser Val Ala Pro Pro Gly Glu Ser Leu Gln Thr Val 290 295 Asn Arg Arg Val Lys Lys Ala Arg Glu Ser Leu Gln Arg Glu Tyr Gly Ala Ala Asn Val Leu Val Val Ser His Val Thr Pro Ile Lys Ala Ile 325 Met Arg Gln Ala Leu Asp Ala Gly Pro Ser Phe Phe Gln Lys Ala His Leu Asp Leu Ala Ser Leu Ser Ile Ala Glu Phe Tyr Glu Asp Gly Pro Thr Cys Val Arg Leu Phe Asn Asp Thr Ser His Leu Glu Ala 375 <210> 47 <211> 840 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(817) <223> RXA02492 <400> 47 gctgtacaac gacgctattg ccaacgaaaa tgtcgacggt gaaacgcatc acggctaagt 60 aaacgcgcgt cgtggaacat aaagtggcaa actagtacct atg act aac gga aaa 115 Met Thr Asn Gly Lys ttg att ctt ctt cgt cac ggt cag agc gaa tgg aac gca tcc aac cag 163 Leu Ile Leu Leu Arg His Gly Gln Ser Glu Trp Asn Ala Ser Asn Gln 10 ttc act gga tgg gtc gac gtc aat ctg acc gaa cag ggt gag gct gag 211 Phe Thr Gly Trp Val Asp Val Asn Leu Thr Glu Gln Gly Glu Ala Glu 25 gcc aaa ggc gtc ctc cca ggc gtt gta tac acc tcc ttg ctg cgc 259 Ala Lys Gly Val Leu Pro Gly Val Val Tyr Thr Ser Leu Leu Arg Arg 40 45 gcg atc cgc act gca aac atc gca ctg aac gct gca gac cgc cac tgg 307 Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala Ala Asp Arg His Trp 55 60 atc cca gtg atc cgc gac tgg cgc ctc aac gag cgt cac tac ggc gca 355 Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu Arg His Tyr Gly Ala 70 75 80

_	_			_	_	_	gca Ala		_	- ,				_	-	403
_		_	_		_	_	tcc Ser		-							451
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	_	_	_		_		gaa Glu	_		_	_	_		_	_	547
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ctc																840

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<212> PRT

<213> Corynebacterium glutamicum

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Gln Gly Glu Ala Glu Ala Lys Gly Val Leu Pro Gly Val Val Tyr Thr 35 40 45

Ser Leu Leu Arg Arg Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala 50 55 60

Ala Asp Arg His Trp Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu Gln Gly Leu Asp Lys Ala Ala Thr Lys Glu 85 90 Lys Tyr Gly Asp Asp Gln Phe Met Glu Trp Arg Arg Ser Tyr Asp Thr 105 Pro Pro Pro Glu Leu Ala Asp Asp Ala Glu Tyr Ser Gln Ala Asn Asp 115 120 Pro Arg Tyr Ala Asp Leu Asp Val Val Pro Arg Thr Glu Cys Leu Lys 135 Asp Val Val Arg Phe Val Pro Tyr Phe Glu Glu Glu Ile Leu Pro 145 150 Arg Ala Lys Lys Gly Glu Thr Val Leu Ile Ala Ala His Gly Asn Ser 165 Leu Arg Ala Leu Val Lys His Leu Asp Gly Ile Ser Asp Ala Asp Ile Ala Glu Leu Asn Ile Pro Thr Gly Ile Pro Leu Val Tyr Glu Ile Ala 200 Glu Asp Gly Ser Val Val Asn Pro Gly Gly Thr Tyr Leu Asp Pro Glu Ala Ala Ala Ala Gly Ala Ala Ala Val Ala Asn Gln Gly Asn Lys 230 225 <210> 49 <211> 729 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(706) <223> RXA00381 <400> 49 aaacctggtt tgtgtcttcc gctctcacgg acgatgattt ctccaagatc gagcaggcac 60 tcaagcccgc cgcacgtgca gcagcagaag cgaaggcatc atg acg caa acc att Met Thr Gln Thr Ile gtc cat cta gtt cgc cac ggc gaa gtc cac aac cca gag aaa atc ctg 163 Val His Leu Val Arg His Gly Glu Val His Asn Pro Glu Lys Ile Leu 10 15 tac gga cgc atg ccc gga tac agg ttg tct tcc cgt gga cgc agc caa 211 Tyr Gly Arg Met Pro Gly Tyr Arg Leu Ser Ser Arg Gly Arg Ser Gln 25 30 gcc gcc cgc act gca gct tct ttt gaa ggc cac gat gtc acc tac att 259 Ala Ala Arg Thr Ala Ala Ser Phe Glu Gly His Asp Val Thr Tyr Ile

40 45 50 gcg gcc tcc cca ttg cag cgt gtg cag gaa acc tcc gaa ccg ttc atc 307 Ala Ala Ser Pro Leu Gln Arg Val Gln Glu Thr Ser Glu Pro Phe Ile 55 60 aag gtc aca ggc cta gaa ctg atc acc gac gag gat ctt ctg gaa gca 355 Lys Val Thr Gly Leu Glu Leu Ile Thr Asp Glu Asp Leu Leu Glu Ala 70 ggc aac cgt ttc gaa ggc ctg cgc acc aaa ggt tgg cgt tcc cag ttg 403 Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly Trp Arg Ser Gln Leu tgg aac ccc gtg cgt tgg cct ttg atg tac aac ccc acg ctt ccc agc 451 Trp Asn Pro Val Arg Trp Pro Leu Met Tyr Asn Pro Thr Leu Pro Ser 105 tgg ggc gaa cac tac acc gac att ttg gaa aga atg atg gcg gct gtg 499 Trp Gly Glu His Tyr Thr Asp Ile Leu Glu Arg Met Met Ala Ala Val 120 gaa cga gct cgg gtg gca gcg gaa gga cac gaa gca atc ctg gtg acc 547 Glu Arg Ala Arg Val Ala Ala Glu Gly His Glu Ala Ile Leu Val Thr 135 cac cag ttg ccg atc gtg tgc gtg caa cgc cac gcc cgc gga caa agc 595 His Gln Leu Pro Ile Val Cys Val Gln Arg His Ala Arg Gly Gln Ser ctg tcc cat aac cca gcg acc agg caa tgc gac ctc gcc tca gtg aca 643 Leu Ser His Asn Pro Ala Thr Arg Gln Cys Asp Leu Ala Ser Val Thr 170 tcc ttg gtg ttc caa gac gat caa att gtc ggc gtg cat tac aac gaa 691 Ser Leu Val Phe Gln Asp Asp Gln Ile Val Gly Val His Tyr Asn Glu 190 cca gct cag gag att tgatcactcg tgcgtttgac caa 729 Pro Ala Gln Glu Ile 200 <210> 50 <211> 202 <212> PRT <213> Corynebacterium glutamicum <400> 50 Met Thr Gln Thr Ile Val His Leu Val Arg His Gly Glu Val His Asn 1.0 Pro Glu Lys Ile Leu Tyr Gly Arg Met Pro Gly Tyr Arg Leu Ser Ser Arg Gly Arg Ser Gln Ala Ala Arg Thr Ala Ala Ser Phe Glu Gly His 40 Asp Val Thr Tyr Ile Ala Ala Ser Pro Leu Gln Arg Val Gln Glu Thr 55

1

Ser Glu Pro Phe Ile Lys Val Thr Gly Leu Glu Leu Ile Thr Asp Glu Asp Leu Leu Glu Ala Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly Trp Arg Ser Gln Leu Trp Asn Pro Val Arg Trp Pro Leu Met Tyr Asn Pro Thr Leu Pro Ser Trp Gly Glu His Tyr Thr Asp Ile Leu Glu Arg 115 120 Met Met Ala Ala Val Glu Arg Ala Arg Val Ala Ala Glu Gly His Glu 135 Ala Ile Leu Val Thr His Gln Leu Pro Ile Val Cys Val Gln Arg His 155 150 Ala Arg Gly Gln Ser Leu Ser His Asn Pro Ala Thr Arg Gln Cys Asp 170 Leu Ala Ser Val Thr Ser Leu Val Phe Gln Asp Asp Gln Ile Val Gly 185 Val His Tyr Asn Glu Pro Ala Gln Glu Ile <210> 51 <211> 822 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(799) <223> RXA02122 <400> 51 ggccttcagc tcaccgacag tttgtacatt tggtggaaga ctcacacccc acaccctaga 60 ccttttttta agtgggcggt caggaatttt tcgcacaggt atg ctg cat gtc atg 115 Met Leu His Val Met aag eeg ggt tea eac gea get gee gaa aag act eaa tee act gtg gtt 163 Lys Pro Gly Ser His Ala Ala Ala Glu Lys Thr Gln Ser Thr Val Val 10 15 tta etc att egg cat ggg caa ace eca aca act ggt eag gtt etg eet 211 Leu Leu Ile Arg His Gly Gln Thr Pro Thr Thr Gly Gln Val Leu Pro 25 30 35 ggt cag acg ccg ggt tta cac ctg tct gat aag ggt gaa gag cag gcg 259 Gly Gln Thr Pro Gly Leu His Leu Ser Asp Lys Gly Glu Glu Gln Ala 40 45 cgg gag gtg gca cag cgt ctg gcg gag gtg ccg att acc gct gtg tat 307 Arg Glu Val Ala Gln Arg Leu Ala Glu Val Pro Ile Thr Ala Val Tyr 55

					cgt Arg 75											355
_				~ ~	ttg Leu	_		_					_	_	_	403
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			-		cag Gln	_		_								499
					gaa Glu											547
					cat His 155											595
_	_	_		_	gct Ala			_			_				_	643
					att Ile											691
			-		tct Ser							-	-	_		739
					tcg Ser											787
-	ccg Pro			tgat	caco	ctc a	accat	ttga	ag c	gc						822
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Gly	Gln	Val 35		Pro	Gly	Gln	Thr 40		Gly	Leu	His	Leu 45		Asp	Lys	
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Ala	Pro	Thr	Val	Ser 85	Ala	His	Gly	Leu	Glu 90	Leu	Thr	Val	Glu	Pro 95	Gly	
Leu	Ile	Glu	Cys 100	Asp	Phe	Gly	Glu	Trp 105	Thr	Gly	Arg	Lys	Leu 110	Thr	Glu	
Leu	Asn	Ala 115	Leu	Glu	Glu	Trp	Lys 120	Ala	Val	Gln	Lys	Thr 125	Pro	Ser	Thr	
Phe	Arg 130	Phe	Pro	Gly	Gly	Glu 135	Ser	Phe	Val	Glu	Met 140	Gln	Asp	Arg	Met	
Val 145	Glu	Ala	Ile	Gly	Asn 150	Ile	Ala	Gln	Gln	His 155	Pro	Gly	Glu	Ile	Val 160	
Ala	Ala	Phe	Ser	His 165	Ala	Asp	Thr	Ile	Lys 170	Ala	Ala	Val	Ala	His 175	Phe	
Val	Gly	Thr	Pro 180	Leu	Asp	Ser	Phe	Gln 185	Arg	Ile	Phe	Ile	Asp 190	Thr	Ala	
Ser	Ile	Ser 195	Ala	Val	Glu	Phe	Thr 200	Gly	Lys	Ser	Ser	Gly 205	Val	Ser	Ser	
His	Met 210	Leu	Leu	Thr	Asn	Ser 215	Arg	Thr	Gly	Ser	Leu 220	Gly	Tyr	Leu	Arg	
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tggg	gtgat	tg t	tcc	ggcgo	eg go	gtgtt	gtga	a tg	ggttt	:aat			gac Asp			115
					tca Ser											163
					cgc Arg											211

						tgg Trp										259
_	_		_	-	_	gat Asp 60		-	_				_			307
						cgc Arg										355
	_	_		_	_	aac Asn		_	_	_			_	_		403
						gga Gly										451
_					-	gtc Val		_		_			_		_	499
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						cgc Arg										595
						gtc Val										643
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_			_		-	gag Glu		_	_		_	_	-	_		739
						ggc Gly 220										787
						gag Glu										835
						gga Gly										883
		_				gat Asp	_	_	_		_					931
caa	cgt	ggt	gga	acc	cca	act	gct	ttc	gac	cgt	gtt	ctg	gcc	act	cgt	979

Gln	Arg	Gly 280	Gly	Thr	Pro	Thr	Ala 285	Phe	Asp	Arg	Val	Leu 290	Ala	Thr	Arg	
		-	_	-	_	_	gcg Ala	_		-		-		-	_	1027
_	_	_	_	_			agc Ser			-				-	-	1075
_	_			_	_	_	gtt Val			_	_		_		_	1123
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Phe Gly Ser Thr Val Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu 35 40 45

Gly Asp Arg Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile
50 55 60

Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp
65 70 75 80

Lys Phe Lys Ala GIy Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala 85 90 95

Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly 100 105 110

Ala Lys Trp Leu Ser Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys
115 120 125

Thr Ile Asp Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp 130 135 140

Thr Ala Val Ala Val Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr 145 150 155 160

Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His 165 170 175

Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr 180 185 190

Thr Val Ile Pro Glu Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala 195 200 Met Glu Arg Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val Ala Glu Gly Ala Leu Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly His Ile Asp Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln 250 Ile Ala Asp Glu Ile His Val Arg Leu Gly His Asp Val Arg Thr Thr Val Leu Gly His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg Val Leu Ala Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu Gly Ser Phe Asp Lys Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met Ile Thr Phe Glu Glu Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu Arg Trp Val Thr Ala Gln Ala Met Phe Gly <210> 55 <211> 1083 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1060) <223> RXA01243 <400> 55 gcgcaatcag cgatatcgat gtggtggtca ccgatgcggg tgcaccagca agtttcgttg 60 agcagttgcg agaacgcgat gtagaagttg tgattgcaga atg att ctt aca gtc 115 Met Ile Leu Thr Val 1 act gca agt ccg tat ctg ttg agc acc aat gag ctt gac ggc acc atc 163 Thr Ala Ser Pro Tyr Leu Leu Ser Thr Asn Glu Leu Asp Gly Thr Ile 10 gaa att ggc gaa gca aac aaa atc cgg cag gtt tcc act gtt gcc ggt 211 Glu Ile Gly Glu Ala Asn Lys Ile Arg Gln Val Ser Thr Val Ala Gly 25 ggt ttt ggc acc ggt gtg gct gcc acc ttg ttt tat ggc ggc aat gaa 259 Gly Phe Gly Thr Gly Val Ala Ala Thr Leu Phe Tyr Gly Gly Asn Glu

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	-		-		_			-	att Ile		_		_			355
									gca Ala 95							403
		-			_		_	-	gtg Val		_	-	_			451
									gat Asp							499
	-			_					gct Ala					_		547
	_			_	_				cat His		_	_	_		_	595
-			_		_	_		-	att Ile 175	_	_		_	_	-	643
									gaa Glu							691
									cca Pro							739
									tta Leu							787
									gaa Glu							835
									agc Ser 255							883
									gga Gly							931
									atc Ile							979
aac	gct	gaa	ggc	agt	gag	tgg	gac	aac	tac	att	ccc	aca	ccc	gat	aag	1027

Asn Ala Glu Gly Ser Glu Trp Asp Asn Tyr Ile Pro Thr Pro Asp Lys 295 300 305

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aaa 1083

<210> 56

<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 56

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Leu Asp Gly Thr Ile Glu Ile Gly Glu Ala Asn Lys Ile Arg Gln Val 20 25 30

Ser Thr Val Ala Gly Gly Phe Gly Thr Gly Val Ala Ala Thr Leu Phe 35 40 45

Tyr Gly Gly Asn Glu Thr Phe Ala Val Phe Pro Ala Pro Glu Ile Ser 50 55 60

His Tyr Met Arg Leu Val Thr Phe Ala Gly Leu Pro His Glu Ile Ile 65 70 75 80

Pro Val Ala Gly Pro Ile Pro Met His Leu Thr Met Arg Asp Ala Glu 85 90 95

Gly Asn Glu Thr Lys Phe Lys Asp Ser Pro Met Pro Leu Asp Val Ser 100 105 110

Gln Leu Ala Ile Leu Arg Asp Leu Val Val Arg Arg Ala Glu Asp Ala 115 120 125

Ala Trp Val Leu Gly Gly Asn Leu Pro Ser Ile Ala Pro Ala Ala 130 135 140

Trp Phe Val Asp Val Val Arg Ser Leu Arg Leu Tyr His Pro His Val 145 150 155 160

Lys Val Ala Ile Ala Ala Thr Gly Ala Ala Leu Arg Ala Val Ile Arg
165 170 175

Gln Leu Ala Ala Thr Ser Pro Asp Ala Leu Ile Val Ala Ala Glu Glu 180 185 190

Ile Glu Ile Ala Thr Gly Leu Glu Pro Lys Thr Leu Arg Gly Pro Trp 195 200 205

Val Glu Gly Asp Leu Ser Pro Thr Val Ala Ala Ala Arg Ala Leu Ile 210 215 220

Asp Ser Gly Val Thr Glu Val Leu Val Thr Asn Lys Arg Thr Glu Ser 225 230 235 240

Leu Tyr Val Ser Glu Ser Glu Ser Leu Leu Ala Ser Tyr Asp Ser Thr 245 250 255

Pro Gly Lys Gln Gly Val Asn Trp Arg Glu Ser Phe Thr Ala Gly Phe 260 265 270

Leu Ala Ala Ser Asn Asp Gly Lys Ser Thr Glu Asp Ser Val Ile Asn 275 280 285

Ala Val Ala Tyr Ala Asn Ala Glu Gly Ser Glu Trp Asp Asn Tyr Ile 290 295 300

Pro Thr Pro Asp Lys Leu Arg Ala Glu His Val Val Ile Lys Ser Leu 305 310 315 320

<210> 57

<211> 1113

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1090)

<223> RXA01882

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Met Ile Ile Thr Phe

1 5

acc cca aac ccg agt att gat tcc acg ctg tcg ctc ggc gaa gag ctc $\,$ 163 Thr Pro Asn Pro Ser Ile Asp Ser Thr Leu Ser Leu Gly Glu Glu Leu $\,$ 10 $\,$ 15 $\,$ 20

tcc cgt gga tcc gtc caa cga ctt gat tcc gtc acc gct gtc gca ggt 211 Ser Arg Gly Ser Val Gln Arg Leu Asp Ser Val Thr Ala Val Ala Gly

ggt aaa ggc atc aat gtc gcc cac gct gtc ttg ctt gcg ggc ttt gaa $$ 259 Gly Lys Gly Ile Asn Val Ala His Ala Val Leu Leu Ala Gly Phe Glu $$ 40 $$ 45 $$ 50

acc ttg gct gtg ttc cca gcc ggc aag ctc gac ccc ttc gtc cca ctg
Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp Pro Phe Val Pro Leu

gtc cgc gac atc ggc ttg ccc gtg gaa act gtt gtg atc aac aag aac 355 Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val Val Ile Asn Lys Asn

gtc cgc acc acc aca gtc acc gaa ccg gac ggc acc acc acc aag 403 Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp Gly Thr Thr Thr Lys 90 95 100

ctc aac ggc ccc ggc gcg ccg ctc agc gag cag aag ctc cgt agc ttg 451

Leu	Asn	Gly	Pro 105	Gly	Ala	Pro	Leu	Ser 110	Glu	Gln	Lys	Leu	Arg 115	Ser	Leu	
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							ggg Gly									547
		_	_				gca Ala	_		_	_	_		-	-	595
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							ctg Leu 285									979
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<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 58

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Thr Ala Val Ala Gly Gly Lys Gly Ile Asn Val Ala His Ala Val Leu 35 40 45

Leu Ala Gly Phe Glu Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp
50 55 60

Pro Phe Val Pro Leu Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val 65 70 75 80

Val Ile Asn Lys Asn Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp 85 90 95

Gly Thr Thr Lys Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln
100 105 110

Lys Leu Arg Ser Leu Glu Lys Val Leu Ile Asp Ala Leu Arg Pro Glu 115 120 125

Val Thr Trp Val Val Leu Ala Gly Ser Leu Pro Pro Gly Ala Pro Val 130 135 140

Asp Trp Tyr Ala Arg Leu Thr Ala Leu Ile His Ser Ala Arg Pro Asp 145 150 155 160

Val Arg Val Ala Val Asp Thr Ser Asp Lys Pro Leu Met Ala Leu Gly
165 170 175

Glu Ser Leu Asp Thr Pro Gly Ala Ala Pro Asn Leu Ile Lys Pro Asn 180 185 190

Gly Leu Glu Leu Gly Gln Leu Ala Asn Thr Asp Gly Glu Glu Leu Glu 195 200 205

Ala Arg Ala Ala Gln Gly Asp Tyr Asp Ala Ile Ile Ala Ala Asp 210 215 220

Val Leu Val Asn Arg Gly Ile Glu Gln Val Leu Val Thr Leu Gly Ala 225 230 235 240

Ala Gly Ala Val Leu Val Asn Ala Glu Gly Ala Trp Thr Ala Thr Ser 245 250 255

Pro Lys Ile Asp Val Val Ser Thr Val Gly Ala Gly Asp Cys Ala Leu 260 265 270

Ala Gly Phe Val Met Ala Arg Ser Gln Lys Lys Thr Leu Glu Glu Ser 275 280 285

Leu Leu Asn Ala Val Ser Tyr Gly Ser Thr Ala Ala Ser Leu Pro Gly 290 295 300

135

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140

145

BGI-126CP - 84 -

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							gag Glu									643
							aag Lys									691
							gca Ala 205									739
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							aag Lys									835
		-		_			ggt Gly						_	-	-	883
	-			_			ggc Gly	_		_	_		-	_		931
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_		-		_			atg Met	_	_	_		_	-	_		1075
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<211> 344

<212> PRT

<213> Corynebacterium glutamicum

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Lys Glu Gly Gly Phe Ala Phe Pro Ala Ile Asn Cys Thr Ser Ser Glu 20 25 30

Thr Ile Asn Ala Ala Leu Lys Gly Phe Ala Glu Ala Glu Ser Asp Gly 35 40 45

Ile Ile Gln Phe Ser Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala 50 55 60

Val Lys Asn Lys Val Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His 65 70 75 80

Glu Ala Ala Lys Ser Tyr Gly Ile Asn Val Ala Leu His Thr Asp His

Cys Gln Lys Glu Val Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile 100 105 110

Ser Gln Glu Arg Val Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His 115 120 125

Met Trp Asp Gly Ser Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala 130 135 140

Gln Glu Leu Leu Ala Lys Ala Lys Ala Asn Ile Ile Leu Glu Val 145 150 155 160

Glu Ile Gly Val Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala 165 170 175

Gly Ala Asn Leu Tyr Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp 180 185 190

Ala Ile Gly Thr Gly Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe 195 200 205

Gly Asn Val His Gly Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro 210 215 220

Glu Val Leu Leu Glu Gly Gln Gln Val Ala Arg Lys Leu Gly Leu 225 230 235 240

Ala Asp Asp Ala Leu Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly 245 250 255

Ser Glu Lys Glu Lys Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys 260 265 270

Met Asn Val Asp Thr Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val 275 280 285

Ser His Met Phe Glu Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu 290 295 300

Val Gly Asn Lys Lys Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala 305 310 315 320

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aac a Asn T																643
gtt g Val A	-		_	_	_	_	-	-		_	-	_		_		691
ctg a Leu I					_		-		-	_			_	_		739
ctt t Leu I					_	_	_	_		-	_			-		787
cag c Gln E 230		_	_	_				-			_			_		835
gaa g Glu <i>F</i>	_		_	_	_	_	_		_		_	_	_			877
taaag	gtac	cag a	agctt	taaa	ag ca	ac										900
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Val Glu Tyr Val Val Glu Gln Thr Arg Lys Ser Leu Ala Gly Leu Asp

145 150 155 160 Ala Ala Glu Leu Ala Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala 165 170 Ile Gly Thr Gly Lys Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys 180 185 Lys Ala Ile Arg Gly Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala Glu Gly Leu Arg Ile Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val 215 Ala Glu Ile Val Gly Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly Ala Ser Leu Asp Gly Glu Ala Phe Ala Lys Leu Ala Ala Asn Ala Ala 245 250 Ser Val Ala <210> 63 <211> 1563 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1540) <223> RXN01225 <400> 63 tttgggctaa tgttgggggg agtgctttca actatccacg agagctgccc agtgataaac 60 cccgggttaa ccccacgcct aagtcagtga aggacttttt atg acg cac aac cac Met Thr His Asn His aag gac tgg aac gat cgc att gca gtt gcg gag gaa atg gtg ccg ttg 163 Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu 10 ate ggg ege etg cae ege aac aac gtg gtg gtt tee gta tte ggt 211 Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly 25 30 cgt ctc ctt gtg aat gtc tca gac atc gat atc atc aag tct cac cgc 259 Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Lys Ser His Arg 40 45 tac gcc cgc cac atc ata tcc aag gaa ctt cca ctg gaa agc tcc ttg 307 Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu 55 60 gat att ttg cgc gaa ctg gta gat atg aac ctt ggt acc gca tcg atc 355 Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu Gly Thr Ala Ser Ile 70 75 80

	ctg Leu															403
	cgt Arg															451
	gac Asp					_			_					_		499
	cgc Arg 135															547
	gct Ala															595
_	gtc Val	_	_	_		_	-	-	_	-		-				643
	gat Asp															691
	ggc Gly															739
_	tac Tyr 215		_					_	_	_		_	_			787
	cgc Arg		-	-	_	-		_		-			_		-	835
	gtt Val															883
	atc Ile								_			-	_	_	_	931
	gtt Val															979
	gtg Val 295															1027
_	cac His					_	_		_		-					1075
ggt	tct	cgc	cgt	ggt	cgc	gca	gca	ggt	ctg	aat	atg	gtt	ctc	acc	gaa	1123

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Gly	Ser	Arg	Arg	Gly 330	Arg	Ala	Ala	Gly	Leu 335	Asn	Met	Val	Leu	Thr 340	Glu	
		_	_	-	-	-		_					_	gaa Glu		1171
_					_		_	_				-		tcc Ser	_	1219
														gag Glu		1267
				_	_			_			-	_	_	cag Gln		1315
	_			_				-	_			_		gtg Val 420		1363
						_	_			_			_	acc Thr		1411
_		_							_					tac Tyr		1459
	_	_		_		-				_			-	cct Pro	-	1507
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cac																1563

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<211> 480

<212> PRT

<213> Corynebacterium glutamicum

<400> 64

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Glu Met Val Pro Leu Ile Gly Arg Leu His Arg Asn Asn Asn Val Val 20 25 30

Val Ser Val Phe Gly Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile 35 40 45

Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro 50 55 60

Leu Glu Ser Ser Leu Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu

70 75 80 65 Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro 100 105 Val Ile Gly Ala Glu Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr 120 Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg 135 Glu Ala Leu Tyr Asp Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys Asn Gly Glu Glu Asp Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn 185 Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn Asp Pro Ala Thr Ile Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln 235 His Leu Lys Ser Lys Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly Lys Gly Asp Leu Lys Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile Thr Ala Asp Asp Gln Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile Asp Asn Phe His Lys Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn 330 Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu 340 345 Pro Glu Leu Glu Gly Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr 360 Pro Asp Val Ser Met Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val 375 370 Asp Arg Asp Glu Val Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser 390 395

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								ctc Leu 110								451
						-		gtg Val						-		499
	_	_	_	_	_		_	gtt Val		-		_	_		-	547
								gtc Val								595
								cgt Arg								643
	_						_	tat Tyr 190	_						_	691
						_		tac Tyr			_		_			739
_			-					gac Asp	_	_		_	_			787
								ctg Leu								835
								gcg Ala								883
								acc Thr 270								931
	-		-	_		_		acc Thr		-						979
								gtg Val								1027
								aac Asn								1075
								ggt Gly								1123
acc	ggc	gct	gca	aag	gct	gta	tcc	aag	gcg	ctt	сса	gag	ctg	gaa	ggc	1171

65

Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly 345 350 355	
aag ctc acc ggc aat gcc atc cgc gtt cct acc cct gac gtg tcc atg 1 Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met 360 365 370	219
gct gtg ctc aac ttg acc ctg aac acg gag gtg gac cgc gat gag gtc 1 Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val 375 . 380 385	267
aac gag ttc ctc cgc cgt gtg tcc ctg cac tct gac ttg cgc cag caa 1 Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln 390 395 400 405	315
atc gac tgg atc cgt tcc cca gag gtt gtt tcc act gac ttc gtg ggc 1 Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly 410 415 420	363
acc acc cac gcg ggc atc gtt gat ggt cta gcc acc atc gca acc ggt 1 Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly 425 430 435	411
cgc cac ctg gtg ctt tac gtg tgg tac gac aac gag ttc ggc tac tcc 1 Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn Glu Phe Gly Tyr Ser 440 445 450	459 [.]
aac cag gtc att cgc atc gtc gag gag atc gcc ggc gtg cgt cct cgc 1 Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala Gly Val Arg Pro Arg 455 460 465	507
gtg tac ccg gag cgc agg cag cca gcc gta cta taggttatcc aagcctaata 1 Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu 470 475 480	560
cac 1	563
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Glu Met Val Pro Leu Ile Gly Arg Leu His Arg Asn Asn Val Val 20 25 30	
Val Ser Val Phe Gly Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile 35 40 45	
Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro 50 55 60	

Leu Glu Ser Ser Leu Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu

Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu

90

70

Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro 100 105 Val Ile Gly Ala Glu Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr 120 Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg 135 Glu Ala Leu Tyr Asp Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys Asn Gly Glu Glu Asp Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn Asp Pro Ala Thr Ile Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln His Leu Lys Ser Lys Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly Lys Gly Asp Leu Lys Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile Thr Ala Asp Asp Gln Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe 295 Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile 310 315 Asp Asn Phe His Lys Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val 370 375 Asp Arg Asp Glu Val Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser 395 390

Asp Leu Arg Gln Gln Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser

410

405

475

Thr Asp Phe Val Gly Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala 420

Thr Ile Ala Thr Gly Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn 435

Glu Phe Gly Tyr Ser Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala 450

Gly Val Arg Pro Arg Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu

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				gca Ala								499
				tac Tyr 140								547
	-	_		aac Asn	_	_		_	_	_	_	595
				gag Glu								643
				ctg Leu								691
				gtc Val								739
				gtt Val 220								787
				cca Pro								835
				gag Glu								883
				ggc Gly								931
_		_	-	acc Thr	_	_		_				979
				acc Thr 300								1027
				gag Glu								1075
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cgt												1125

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<213> Corynebacterium glutamicum

<400> 68

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Val Asn Asp Leu Thr Asp Asn Lys Thr Leu Ser Thr Leu Leu Lys Phe $35 \hspace{1cm} 40 \hspace{1cm} 45$

Asp Ser Ile Met Gly Arg Leu Gly Gln Glu Val Glu Tyr Asp Asp 50 55 60

Ser Ile Thr Val Gly Gly Lys Arg Ile Ala Val Tyr Ala Glu Arg Asp 65 70 75 80

Pro Lys Asn Leu Asp Trp Ala Ala His Asn Val Asp Ile Val Ile Glu 85 90 95

Ser Thr Gly Phe Phe Thr Asp Ala Asn Ala Ala Lys Ala His Ile Glu 100 105 110

Ala Gly Ala Lys Lys Val Ile Ile Ser Ala Pro Ala Ser Asn Glu Asp 115 120 125

Ala Thr Phe Val Tyr Gly Val Asn His Glu Ser Tyr Asp Pro Glu Asn 130 135 140

His Asn Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro 145 150 155 160

Met Ala Lys Val Leu Asn Asp Lys Phe Gly Ile Glu Asn Gly Leu Met 165 170 175

Thr Thr Val His Ala Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro 180 185 190

His Arg Asp Leu Arg Ala Arg Ala Ala Ala Val Asn Ile Val Pro 195 200 205

Thr Ser Thr Gly Ala Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu 210 215 220

Lys Gly Lys Leu Asp Gly Tyr Ala Leu Arg Val Pro Val Ile Thr Gly 225 230 235 240

Ser Ala Thr Asp Leu Thr Phe Asn Thr Lys Ser Glu Val Thr Val Glu 245 250 255

Ser Ile Asn Ala Ile Lys Glu Ala Ala Val Gly Glu Phe Gly Glu 260 265 270

Thr Leu Ala Tyr Ser Glu Glu Pro Leu Val Ser Thr Asp Ile Val His 275 280 285

Asp Ser His Gly Ser Ile Phe Asp Ala Gly Leu Thr Lys Val Ser Gly 290 295 300

Asn Thr Val Lys Val Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr 305 310 315 320

Cys Gln Leu Leu Arg Leu Thr Glu Leu Val Ala Ser Lys Leu $325 \hspace{1cm} 330$

<210> 69

<211> 1338

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1315)

<223> RXA02257

<400> 69

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			cgc cac gtc atc gtt 1 Arg His Val Ile Val 20	63
	Asn Val Pro		cgc gag atc acc gat 2 Arg Glu Ile Thr Asp 35	11
	-		aaa gca ctg agc gaa 2 Lys Ala Leu Ser Glu 50	:59
			ggc cgc cca aag ggc 3 Gly Arg Pro Lys Gly 65	07
			gct gag gca ctc tcc 3. Ala Glu Ala Leu Ser 85	55
			gac gtt gtt ggc gaa 40 Asp Val Val Gly Glu 100	03
	Arg Ala Asn		ggc gac atc ctg ctc 49 Gly Asp Ile Leu Leu 115	51
			tcc aag gac gag gca 4 Ser Lys Asp Glu Ala 130	99
			ctt gca gca gac aac 5. Leu Ala Ala Asp Asn 145	47
ggc gca ttc gtt	tct gac ggc	ttc ggt gtt gtc	cac ege gea eag acc 5	95

Gly 150	Ala	Phe	Val	Ser	Asp 155	Gly	Phe	Gly	Val	Val 160	His	Arg	Ala	Gln	Thr 165	
	_		_		_	aag Lys	_	_				-			_	643
_						gtt Val	_	_	_		_	-				691
						ctc Leu										739
						gct Ala 220										787
						ttc Phe										835
						gaa Glu										883
						atc Ile										931
	_			_	-	gca Ala		_	_		_	_	_	_		979
		_			_	tct Ser 300		_						-	_	1027
						agc Ser										1075
						ttc Phe										1123
	_	-	_			gat Asp	_		_			_	_			1171
						tcc Ser										1219
						cac His 380										1267
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1338

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Cys Thr Asp Leu Leu Ala Arg Phe Gly Asp Lys Ile Val Leu Pro Val

265

260

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			gaa Glu							403
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			gat Asp							499
			cac His						atc Ile '	547
			gct Ala 155							595
			gca Ala							643
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			gac Asp							787
			gac Asp 235							835
			ggc Gly							883
			aac Asn							931
			gac Asp							979
			acc Thr							1027

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					ggt Gly 365								1219
					tgt Cys								1267
					aag Lys			_			-		1315
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His Glu Leu Arg Asp Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu 50 55 60

Lys Ala Val Glu Asn Val Asn Glu Glu Ile Gly Asp Glu Leu Ala Gly 65 70 75 80

Leu Glu Ala Asp Asp Gln Arg Leu Ile Asp Glu Ala Met Ile Lys Leu 85 90 95

Asp Gly Thr Ala Asn Lys Ser Arg Leu Gly Ala Asn Ala Ile Leu Gly
100 105 110

Val Ser Met Ala Val Ala Lys Ala Ala Ala Asp Ser Ala Gly Leu Pro

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Met 145	Met	Asn	Ile	Ile	Thr 150	Gly	Gly	Ala	His	Ala 155	Asp	Ser	Gly	Val	Asp 160
Val	Gln	Glu	Phe	Met 165	Ile	Ala	Pro	Ile	Gly 170	Ala	Glu	Thr	Phe	Ser 175	Glu
Ala	Leu	Arg	Asn 180	Gly	Ala	Glu	Val	Tyr 185	His	Ala	Leu	Lys	Ser 190	Val	Ile
Lys	Glu	Lys 195	Gly	Leu	Ser	Thr	Gly 200	Leu	Gly	Asp	Glu	Gly 205	Gly	Phe	Ala
Pro	Ser 210	Val	Gly	Ser	Thr	Arg 215	Glu	Ala	Leu	Asp	Leu 220	Ile	Val	Glu	Ala
Ile 225	Glu	Lys	Ala	Gly	Phe 230	Thr	Pro	Gly	Lys	Asp 235	Ile	Ala	Leu	Ala	Leu 240
Asp	Val	Ala	Ser	Ser 245	Glu	Phe	Phe	Lys	Asp 250	Gly	Thr	Tyr	His	Phe 255	Glu
Gly	Gly	Gln	His 260	Ser	Ala	Ala	Glu	Met 265	Ala	Asn	Val	Tyr	Ala 270	Glu	Leu
Val	Asp	Ala 275	Tyr	Pro	Ile	Val	Ser 280	Ile	Glu	Asp	Pro	Leu 285	Gln	Glu	Asp
qzA	Trp 290	Glu	Gly	Tyr	Thr	Asn 295	Leu	Thr	Ala	Thr	Ile 300	Gly	Asp	Lys	Val
Gln 305	Ile	Val	Gly	Asp	Asp 310	Phe	Phe	Val	Thr	Asn 315	Pro	Glu	Arg	Leu	Lys 320
Glu	Gly	Ile	Ala	Lys 325	Lys	Ala	Ala	Asn	Ser 330	Ile	Leu	Val	Lys	Val 335	Asn
Gln	Ile	Gly	Thr 340		Thr	Glu		Phe 345	Asp	Ala	Val		Met 350	Ala	His
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Lys 385	Thr	Gly	Ala	Pro	Ala 390	Arg	Ser	Asp	Arg	Val 395	Ala	Lys	Tyr	Asn	Gln 400
Leu	Leu	Arg	Ile	Glu 405	Gln	Leu	Leu	Gly	Asp 410	Ala	Gly	Val	Tyr	Ala 415	Gly
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                                            Met Gly Val Asp Arg
cga act aag att gta tgt acc cta ggc cca gcg gtg gct agt gca gat
                                                                   163
Arg Thr Lys Ile Val Cys Thr Leu Gly Pro Ala Val Ala Ser Ala Asp
gga att ctg cgt ttg gta gaa gac ggc atg gat gtt gct cgc ctc aac
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Gly Ile Leu Arg Leu Val Glu Asp Gly Met Asp Val Ala Arg Leu Asn
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Phe Ser His Gly Asp His Pro Asp His Glu Gln Asn Tyr Lys Trp Val
cgc gag gcg gcg gag aag act ggc cgt gca gtc ggt att ctc gca gac
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Arg Glu Ala Ala Glu Lys Thr Gly Arg Ala Val Gly Ile Leu Ala Asp
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Leu Gln Gly Pro Lys Ile Arg Leu Gly Arg Phe Thr Asp Gly Ala Thr
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                                                                   403
Val Trp Glu Asn Gly Glu Thr Ile Arg Ile Thr Val Asp Asp Val Glu
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                                                                   451
Gly Thr His Asp Arg Val Ser Thr Thr Tyr Lys Asn Leu Ala Lys Asp
gcg aag cca ggc gac cgc ctg ctc gtt gat gac ggc aag gtt ggc ctc
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Ala Lys Pro Gly Asp Arg Leu Leu Val Asp Asp Gly Lys Val Gly Leu
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Val Cys Val Ser Val Glu Gly Asn Asp Val Ile Cys Glu Val Val Glu
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ggc gga cca gtc tcc aac aac ggt gtt tcc ctg cca ggt atg gat
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Gly Gly Pro Val Ser Asn Asn Lys Gly Val Ser Leu Pro Gly Met Asp
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att tee gta eet gea etg tee gaa aag gat ate egt gae etg ege tte
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Ile Ser Val Pro Ala Leu Ser Glu Lys Asp Ile Arg Asp Leu Arg Phe
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691

Ala	Leu	Lys	Leu 185	Gly	Val	Asp	Phe	Ile 190	Ala	Leu	Ser	Phe	Val 195	Arg	Ser	
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	gtt Val 215															787
	gag Glu															835
-	ctc Leu		_		_		_			_		_	_	_	-	883
-	gca Ala		_		_	_			_	_		-			-	931
	cag Gln	_	_	_		_					-			_		979
_	gct Ala 295		_		_		-			_		_	_	-	_	1027
_	ctt Leu			_						-	_			_		1075
	acc Thr	-		_		_	_		_	_		_		_	_	1123
	gac Asp	_					_		_	-		-				1171
	gca Ala															1219
	acc Thr 375															1267
	ctg Leu															1315
_	gcg Ala	_				-				_	_			-	-	1363
_	acc Thr	_	_	_	_	_	_	_	_	_	_			_	_	1411

425 430 435 cct gag tac aac aag ggt gac atg atg gtt gtt gtt gca ggt tcc cct 1459 Pro Glu Tyr Asn Lys Gly Asp Met Met Val Val Val Ala Gly Ser Pro 440 cct ggt gtt acc ggt aac acc aac atg att cac gtc cac ctt ctt ggt 1507 Pro Gly Val Thr Gly Asn Thr Asn Met Ile His Val His Leu Leu Gly 455 460 gac gac aca agg att gca aag ctc taatcgctta aatctttcaa aaa 1554 Asp Asp Thr Arg Ile Ala Lys Leu 470 <210> 74 <211> 477 <212> PRT <213> Corynebacterium glutamicum <400> 74 Met Gly Val Asp Arg Arg Thr Lys Ile Val Cys Thr Leu Gly Pro Ala Val Ala Ser Ala Asp Gly Ile Leu Arg Leu Val Glu Asp Gly Met Asp Val Ala Arg Leu Asn Phe Ser His Gly Asp His Pro Asp His Glu Gln Asn Tyr Lys Trp Val Arg Glu Ala Ala Glu Lys Thr Gly Arg Ala Val Gly Ile Leu Ala Asp Leu Gln Gly Pro Lys Ile Arg Leu Gly Arg Phe Thr Asp Gly Ala Thr Val Trp Glu Asn Gly Glu, Thr Ile Arg Ile Thr Val Asp Asp Val Glu Gly Thr His Asp Arg Val Ser Thr Thr Tyr Lys 105 Asn Leu Ala Lys Asp Ala Lys Pro Gly Asp Arg Leu Leu Val Asp Asp Gly Lys Val Gly Leu Val Cys Val Ser Val Glu Gly Asn Asp Val Ile Cys Glu Val Val Glu Gly Gly Pro Val Ser Asn Asn Lys Gly Val Ser 145 Leu Pro Gly Met Asp Ile Ser Val Pro Ala Leu Ser Glu Lys Asp Ile 170 Arg Asp Leu Arg Phe Ala Leu Lys Leu Gly Val Asp Phe Ile Ala Leu 180 185 Ser Phe Val Arg Ser Pro Ala Asp Ala Glu Leu Val His Lys Ile Met 200 Asp Glu Glu Gly Arg Arg Val Pro Val Ile Ala Lys Leu Glu Lys Pro

210 215 220 Glu Ala Val Thr Ser Leu Glu Pro Ile Val Leu Ala Phe Asp Ala Val 230 235 Met Val Ala Arg Gly Asp Leu Gly Val Glu Val Pro Leu Glu Glu Val 245 250 Pro Leu Val Gln Lys Arg Ala Ile Gln Ile Ala Arg Glu Asn Ala Lys 265 Pro Val Ile Val Ala Thr Gln Met Leu Asp Ser Met Ile Glu Asn Ser 275 Arg Pro Thr Arg Ala Glu Ala Ser Asp Val Ala Asn Ala Val Leu Asp Gly Ala Asp Ala Val Met Leu Ser Gly Glu Thr Ser Val Gly Lys Asp 305 310 315 Pro His Asn Val Val Arg Thr Met Ser Arg Ile Val Arg Phe Ala Glu Thr Asp Gly Arg Val Pro Asp Leu Thr His Ile Pro Arg Thr Lys Arg 345 Gly Val Ile Ser Tyr Ser Ala Arg Asp Ile Ala Glu Arg Leu Asn Ala Arg Ala Leu Val Ala Phe Thr Thr Ser Gly Asp Thr Ala Lys Arg Val 375 Ala Arg Leu His Ser His Leu Pro Leu Leu Val Phe Thr Pro Asn Glu 390 395 Ala Val Arg Ser Glu Leu Ala Leu Thr Trp Gly Ala Thr Thr Phe Leu 410 Cys Pro Pro Val Ser Asp Thr Asp Asp Met Met Arg Glu Val Asp Arg 425 Ala Leu Leu Ala Met Pro Glu Tyr Asn Lys Gly Asp Met Met Val Val Val Ala Gly Ser Pro Pro Gly Val Thr Gly Asn Thr Asn Met Ile His Val His Leu Leu Gly Asp Asp Thr Arg Ile Ala Lys Leu 470

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	215					220					225					
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	_			-		cta Leu	_			_	-			_		931
-		-			_	cga Arg	_						_		_	979
		-		_	-	ggc Gly 300				_						1027
		-		His		tac Tyr	-	_			_					1075
_	-	_	_	_		aac Asn			_		_	_				1123
	-	_	-			tac Tyr	_							_		1171
	_		_	_		ctt Leu			-	-		_			_	1219
		_				gac Asp 380	_		_		_	_	_	_		1267
						gac Asp										1315
		_	-			ggc Gly	-		_	-	-		_			1363
			_		_	ctt Leu				_			_	_	_	1411
			_	_		gtc Val	_			_	_		-	_		1459
						gcc Ala 460										1507

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aaa atc gag a Lys Ile Glu T		,,		-		-
acc ggc atg c Thr Gly Met A	-	Asn Phe G				
ctc gcc gtc g Leu Ala Val G 520						
atc atg gcc c Ile Met Ala I 535						
caa gtc ctg g Gln Val Leu G 550	,	_	Asn Gly L			-
atc acc gac g Ile Thr Asp A		-				
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Ala Ile Gly G	Gln Val Ser	Pro Thr H	His Tyr V	al Gly Ala 45	Arg Asn	Leu
Met His Tyr A	Ala His Leu	Arg Thr L	Lys Asp L	Leu Arg Gly 60	Leu Gln	Gln

Arg Leu Ser Ser Val Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala

65 70 75 Val Gln Ala Arg Leu Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala Gly Glu Gly Pro Leu Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu 105 Asp Ala Asp Glu Ile Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu 120 Pro Leu Pro Asp Thr Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu 130 135 Ala Ala Thr Asp Ile Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met Asn Leu Ala Arg Ile Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys Gln Met Ile Asp Asn Val His Thr Val Ala Glu Glu Val Gly Arg Glu Ile Arg Val Ser Met Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu Ile Ala Pro Gly Ala Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu 215 Thr Gly Lys Val Leu Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly 225 235 Ser Glu Pro Val Pro Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu 250 245 Pro Ile Glu Val Thr Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser 265 Val Ile Asn Val Pro Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val Thr Arg Val Phe Asp Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala 295 Tyr Ile Ser Asn Gly Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg Val Tyr Gly Ile Pro Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly 330 Asp Arg Leu Ile Leu Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu Gly Ser Gly Arg Thr Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val 360 Asp Ala Ile Lys Val Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile 375 Ala Ala Val Cys Ile Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp 395 390

Val Glu Leu Glu Val Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala 405 Ala Tyr Lys Gly Ile Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser 425 Leu Thr Glu Glu Asp Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala 435 Asp Ile Ala Ala Ile Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr 455 Leu Leu Gln Ala Leu Ala Asp Ile Gly Asp Pro Val Ala Val Glu Arg 465 Leu Gly Leu Val Leu Lys Ile Glu Thr Ile Pro Gly Tyr Glu Gly Leu Ala Gln Ile Leu Leu Thr Gly Met Arg His Glu Asn Phe Gly Ile Met Ile Ala Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala 520 Glu Val Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro 535 Thr Ile Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu 550 Pro Ser Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val 585 Leu Thr Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu Leu Arg Lys Val Lys Ser Trp Glu Glu 610 615 <210> 77 <211> 386 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(363) <223> FRXA02675 <400> 77 atc ctc atg acc ggc atg cgc cac gaa aac ttc ggc atc atg atc gcc Ile Leu Met Thr Gly Met Arg His Glu Asn Phe Gly Ile Met Ile Ala 1 10

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Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala Glu Val

48

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		tg gca ctt cgc gct gaa tgc gtc 2- let Ala Leu Arg Ala Glu Cys Val 75 80	40
		ac gac gcc atc aag gtc ctc acc 20 sn Asp Ala Ile Lys Val Leu Thr 90 95	88
	Lys Leu Gly Ala Se	cc caa cga aag agt agg ctg ctg 33 er Gln Arg Lys Ser Arg Leu Leu 05 110	36
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cgt		31	86
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Ile Leu Met Thr G 1 Arg Gly Asp Leu F 20 Pro Gln Leu Ile M 35 Leu Ala Thr Gln W	5 Ala Val Glu Leu Gl 2 Met Ala Leu Ala Gl 40 Val Leu Glu Asn Me 55	10 15 Ply Phe Asp Arg Met Ala Glu Val 25 30 Plu Ala Ala His Val Pro Thr Ile 45 et Ala Lys Asn Gly Leu Pro Ser	
Ile Leu Met Thr G 1 Arg Gly Asp Leu F 20 Pro Gln Leu Ile M 35 Leu Ala Thr Gln W 50 Arg Ala Glu Ile T 65	Ala Val Glu Leu Gl 2 Met Ala Leu Ala Gl 40 Val Leu Glu Asn Me 55 Thr Asp Ala Ala Me	10 15 Ply Phe Asp Arg Met Ala Glu Val 25 30 Plu Ala Ala His Val Pro Thr Ile 45 Pet Ala Lys Asn Gly Leu Pro Ser 60 Fet Ala Leu Arg Ala Glu Cys Val	
Ile Leu Met Thr G 1 Arg Gly Asp Leu F 20 Pro Gln Leu Ile M 35 Leu Ala Thr Gln W 50 Arg Ala Glu Ile T 65 Met Leu Asn Lys G	Ala Val Glu Leu Gl Met Ala Leu Ala Gl 40 Val Leu Glu Asn Me 55 Thr Asp Ala Ala Me 70 Gly Pro His Ile As 85	10 15 Aly Phe Asp Arg Met Ala Glu Val 25 30 Alu Ala Ala His Val Pro Thr Ile 45 Ala Lys Asn Gly Leu Pro Ser 60 At Ala Leu Arg Ala Glu Cys Val 75 80 Asp Ala Ile Lys Val Leu Thr	

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                                             Met Asn Glu Phe Asp
cag gac att ctc cag gag atc aag act gaa ctc gac gag tta att cta
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Gln Asp Ile Leu Gln Glu Ile Lys Thr Glu Leu Asp Glu Leu Ile Leu
gaa ctt gat gag gtg aca caa act cac agc gag gcc atc ggg cag gtc
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Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu Ala Ile Gly Gln Val
tcc cca acc cat tac gtt ggt gcc cgc aac ctc atg cat tac gcg cat
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Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu Met His Tyr Ala His
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                             45
ctt cgc acc aaa gac ctc cgt ggc ctg cag caa cgc ctc tcc tct gtg
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Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln Arg Leu Ser Ser Val
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Gly Ala Thr Arg Leu Thr Thr Glu Pro Ala Val Gln Ala Arg Leu
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                                                                   403
Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala Gly Glu Gly Pro Leu
tat cca ccc tca gat gtc gtc gat gcc ttc gaa gat gcc gat gag att
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Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu Asp Ala Asp Glu Ile
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Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu Pro Leu Pro Asp Thr
cca tcc tgc atc atg gtc acc ctg ccc acc gaa gcc gcc acc gac att
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Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu Ala Ala Thr Asp Ile
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gaa ctt gtc cgt ggc ttc gcc aaa agc ggc atg aat cta gct cgc atc
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Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met Asn Leu Ala Arg Ile
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                    155
aac tgt gca cac gac gat gaa acc gtc tgg aag cag atg atc gac aac
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Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys Gln Met Ile Asp Asn
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gtc cac acc gtt gca gaa gaa gtt ggc cgg gaa atc cgc gtc agc atg
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Val	His	Thr	Val 185	Ala	Glu	Glu	Val	Gly 190	Arg	Glu	Ile	Arg	Val 195	Ser	Met	
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						ggt Gly					-		-			883
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		_	_			tac Tyr	_	_			_					1075
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	_	-	_			tac Tyr	-							-		1171
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						gac Asp 380										1267
-	_				_	gac Asp				_		_	_	_	-	1315
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						ctt Leu										1411

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220 210 215 Thr Gly Lys Val Leu Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly 230 235 Ser Glu Pro Val Pro Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu 245 Pro Ile Glu Val Thr Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser Val Ile Asn Val Pro Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val Thr Arg Val Phe Asp Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala 295 Tyr Ile Ser Asn Gly Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg Val Tyr Gly Ile Pro Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly 325 Asp Arg Leu Ile Leu Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu 345 Gly Ser Gly Arg Thr Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val Asp Ala Ile Lys Val Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile 375 Ala Ala Val Cys Ile Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp Val Glu Leu Glu Val Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala Ala Tyr Lys Gly Ile Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser 425 Leu Thr Glu Glu Asp Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala Asp Ile Ala Ala Ile Ser Phe Ile Arg Asn Val Ala Asp Val Glu Tyr 455 Leu Leu Gln Ala Leu Ala Asp Ile Gly Asp

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<223> RXA00682

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		ttc Phe				_							_	_	1027
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		tcc Ser	_	_		_	_			_	-	_	-	_	 1123
	_	gaa Glu		_	_		_	_		_			_	_	1171
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		ttc Phe													1267
		gaa Glu													1315
		gac Asp													1363
		ctg Leu													1411
		atc Ile 440													1459
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				_	gct Ala	_						-			_	1651
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Asp	Lys	Leu 35	Met	Asp	Gln	Glu	Asn 40	Glu	Lys	Phe	Trp	Phe	Cys	Asp	Ser	

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35

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50 55 60

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Pro Asn Ala Asn Gly Ile Glu Phe Arg Val His Leu Gly Tyr Leu Tyr 85 90 95

Met Ser Pro Ile Pro Val Pro Glu Asp Gln Ile Ala Glu Arg Val Pro 100 105 110

Met Phe Gln Glu Arg Ile Thr His Tyr Phe Gln Asn Trp Glu Pro Met 115 120 125

Leu Ala Asn Trp Lys Glu Arg Val Leu Gly Thr Ile Asn Glu Leu Glu 130 135 140

Ser Leu Glu Phe Lys Pro Leu Pro Asp Tyr Val Pro Ile Asp Asp Ile 145 150 155 160

Val Ser Gly Lys Ala Lys Asp Gly Thr Glu Val Leu Met Glu Asn Phe
165 170 175

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Phe Leu Asn Leu Gly Tyr Ile Ala Tyr Leu Asp Phe Phe Asn Phe Cys 195 200 205

Lys Glu Val Phe Pro Asp Ile Pro Asp Gln Ser Ile Ser Met Met Val 210 215 220

Gln Gly Val Asp Met Glu Leu Phe Arg Pro Asp Asp Glu Leu Lys Ile 225 230 235 240

Leu Ala Gln Leu Ala Val Asp Leu Gly Leu Gln Thr His Phe Ala Asn 245 250 255

Pro Asp Asp Pro Gln Ala Thr Leu Ala Ala Ile Ala Lys Ala Glu Gly 260 265 270

Gly Ala Thr Trp Ile Ala Arg Trp Glu Glu Ala Gln Asp Pro Trp Phe 275 280 285

Asn Phe Thr Val Gly Asn Gly Phe Tyr Gly His Asp Lys Tyr Trp Ile 290 295 300

Glu His Leu Glu Leu Pro Leu Gly Tyr Ile Ala Asp Tyr Ile Arg Arg 305 310 315 320

Leu Asp Glu Gly Gln Thr Ile Ser Arg Pro Lys Asp Glu Leu Ile Ala 325 330 335

Glu Lys Glu Arg Val Val Glu Glu Tyr Arg Asp Leu Leu Asp Gly Glu 340 345 350

Gln Leu Ala Gln Phe Asp Ala Lys Cys Gly Leu Ala Ala Thr Ala Tyr 355 360 365

Pro Tyr Val Glu Asn His Asn Phe Tyr Ile Glu His Trp Thr Met Ser

375 370 380 Val Phe Trp Arg Lys Val Arg Glu Leu Ser Arg Thr Leu Gln Gly Tyr 390 395 Gly Phe Trp Glu Asn Glu Asp Asp Met Leu Tyr Leu Asn Arg Thr Glu 405 410 Val Arg Asp Val Leu Phe Asp Leu Ala Thr Ala Trp Gly Val Gly Ala 420 425 Pro Gly Gly Pro Ile Gly Thr Ile Ile Trp Pro Glu Glu Ile Glu Arg Arg Lys Ala Ile Val Thr Ala Leu Lys Thr Ala Arg Pro Ala Pro Ala Leu Asn Thr Pro Pro Glu Ser Ile Thr Glu Pro Phe Thr Arg Met Leu Trp Gly Ile Thr Thr Glu Gln Val Gln Ser Trp Leu Gly Asn Asp Glu Asp Ala Glu Gly Thr Leu Lys Gly Met Ala Ala Ser Pro Gly Val 505 Val Glu Gly Tyr Ala Arg Val Ile Leu Ser Ala Asp Asp Leu Ser Glu Ile Gln Gln Asp Glu Ile Leu Val Ala Pro Val Thr Ala Pro Ser Trp 535 Gly Pro Ile Phe Gly Lys Ile Lys Ala Thr Val Thr Asp Ile Gly Gly Met Met Ser His Ala Ala Ile Val Cys Arg Glu Tyr Gly Leu Pro Ala Val Thr Gly Thr Gly Ala Ala Ser Thr Thr Ile Lys Thr Gly Asp Tyr 585 Leu Lys Val Asp Gly Thr Lys Gly Lys Val Val Ile Val Asp Pro Asp Ala Pro Arg Ile Glu Gly Pro Gly Ala His Ser His Ala His Ser Val Ala Ala His Gly Val Asp Thr His Ala 630

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acc . Thr																931
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aag Lys																1027
ctg (Leu 2 310	-	_	_	_		-		_			_		-			1075
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Pro (_	-	-	Lys	Thr	Ile	Gly	Thr 350	Phe	Asp	Phe	Ser	Ser 355	Ile	Thr	
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						aag Lys									835
						ctg Leu									883
						ctg Leu									931
						gac Asp 285									979
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gta cgc at Val Arg Il	_	_	_		_	_		_		_		-	1651
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Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu 115 Met Val Asn Gly Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile 135 Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Val Ile Pro Gly 145 150 155 Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala 180 Ala Leu Val Glu Ala Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile 230 Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro 310 315 His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys 330 Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn 345 Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg 385 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro 410 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala

425

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Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg 115 120 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro 135 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala 145 155 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Gly Glu Leu Leu Thr 165 170 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser 180 185 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu 265 Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile 295 Pro Thr Pro 305 <210> 91 <211> 954 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(931) <223> RXN03044 <400> 91 tacgccaccc acggcaaggc catgattccg ctgtacatct tctactcgat gttcgggatt 60 ccagcgcacc ggtgactcca tctgggcagc agccgatcag atg gca cgt ggc ttc 115 Met Ala Arg Gly Phe ctc ttg ggc gct acc gca ggt cgc acc acc ctg acc ggt gaa ggc ctc 163 Leu Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu

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Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile
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Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys
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Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg
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                                110
gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca
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Gly Ala Ala
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	acc Thr				_	-										384
	tct Ser 130			_	_	_			_			-	_		-	432
	aag Lys	-	_	_		_		-			_					480
-	ggt Gly	_		_			_	-		_		_		-	_	528
	cac His				_	_		_		_	_		-			576
_	acc Thr	_	_	_			_			_				_		624
_	aag Lys 210	_		_	_		_	_	_				_	_	_	672
	acc Thr				-											720
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	gat Asp															816
	cag Gln															864
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	ggc Gly															960
	cca Pro															1008

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Thr Val Ser M						
35	et Gly Le		o Met Asp 10	Ala Ile Tyr 45	Gln Ala Arg	
		4	10	45		
35 Phe Asn Arg Ty	vr Leu G .a Phe Le	4 lu Asn Ar 55	g Gly Ile	45 Lys Asp Thr 60	Ser Asp Gln	
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Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly 115 Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu 135 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His 235 Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln 325 Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met 345 Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu 355 Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr 375 Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu 385 395 Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn 410 Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala

425

- 149 -

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Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg



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		-			-		acc Thr		_							720
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Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln 50 55 60

His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser 65 70 75 80

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Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly
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Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
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Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu 130 135 140

Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser 145 150 155 160

Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg 165 170 175

Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn 180 185 190

Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr 195 200 205

Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg 210 215 220

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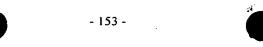
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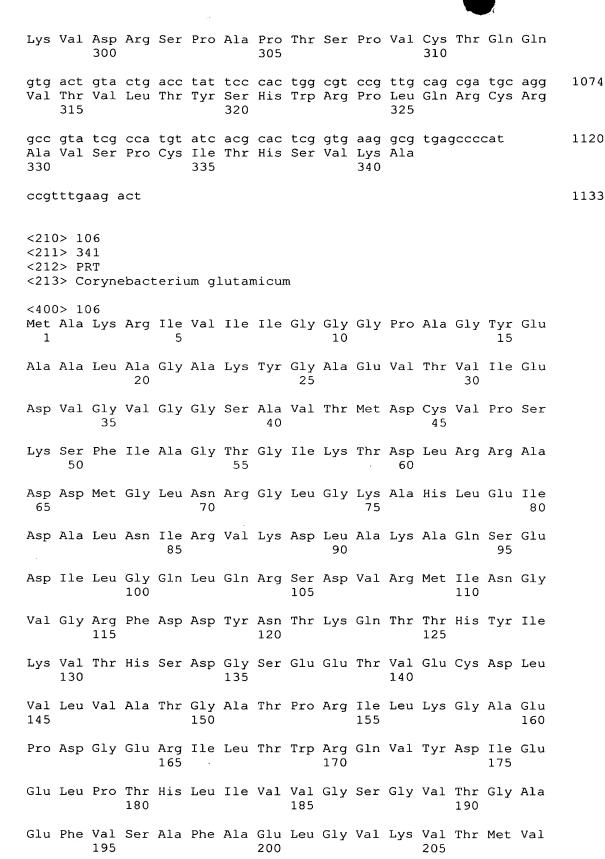
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acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile



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		_			_	atc Ile 80	_	-	_			_		_	-	354
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						ggt Gly										450
						att Ile										498
						ctg Leu										546
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						gtg Val										738
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						cat His 240										834
						gtt Val										882
						act Thr										930
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210



Ala Ser Arg Asp Arg Ile Leu Pro His Asp Asp Ala Asp Ala Ala Asp

220



Val Leu Glu Thr Val Leu Ala Glu Arg Gly Val Ser Leu Glu Lys His 225 230 235 240
Ala Arg Val Glu Ser Val Thr Arg Thr Glu Asp Gly Gly Val Cys Val 245 250 255
Arg Thr Ala Asp Gly Arg Glu Ile Tyr Gly Ser His Ala Leu Met Thr 260 265 270
Val Gly Ser Ile Pro Asn Thr Ala Asp Leu Gly Leu Glu Asn Ile Gly 275 280 285
Val Glu Leu Ala Pro Ser Gly His Ile Lys Val Asp Arg Ser Pro Ala 290 295 300
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gca gaa gtt acc gtt att gaa gat gtc gga gtt ggc gga tcc gca gtc 211 Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val 30 35 40
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gga aaa gca cac cta gaa atc gat gca ctg aac atc cgt gtg aag gac 355 Gly Lys Ala His Leu Glu Ile Asp Ala Leu Asn Ile Arg Val Lys Asp

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					ttt Phe											1315
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1		1	,	5				-	10	_			_	15		
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Lys	Ser 50	Phe	Ile	Ala	Gly	Thr 55	Gly	Ile	Lys	Thr	Asp 60	Leu	Arg	Arg	Ala	
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405 410 415 Val Ala Pro Thr Ala Ser Glu Leu Ile Leu Pro Ile Ala Val Ala Val 425 Thr Asn Arg Leu Thr Val Ala Asp Leu Ala Asp Thr Phe Ala Val Tyr 435 440 Pro Ser Leu Ser Gly Ser Ile Thr Glu Ala Ala Arg Gln Leu Val Gln 455 460 His Asp Asp Leu Gly 465 <210> 109 <211> 2895 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(2872) <223> RXA02259 <400> 109 atgageceat gaaagecate gaaateaate geeeagetaa acaeetgttt tgetgggtga 60 ttttttatct catgcacgcc aacaccctca atgtgaaaga gtg ttt aaa gta gtt 115 Val Phe Lys Val Val atg act gat ttt tta cgc gat gac atc agg ttc ctc ggt caa atc ctc 163 Met Thr Asp Phe Leu Arg Asp Asp Ile Arg Phe Leu Gly Gln Ile Leu 10 ggt gag gta att gcg gaa caa gaa ggc cag gag gtt tat gaa ctg gtc 211 Gly Glu Val Ile Ala Glu Gln Glu Gly Gln Glu Val Tyr Glu Leu Val 259 gaa caa gcg cgc ctg act tct ttt gat atc gcc aag ggc aac gcc gaa Glu Gln Ala Arg Leu Thr Ser Phe Asp Ile Ala Lys Gly Asn Ala Glu 45 atg gat age ctg gtt cag gtt ttc gac ggc att act cca gcc aag gca 307 Met Asp Ser Leu Val Gln Val Phe Asp Gly Ile Thr Pro Ala Lys Ala 55 60 aca ccg att gct cgc gca ttt tcc cac ttc gct ctg ctg gct aac ctg 355 Thr Pro Ile Ala Arg Ala Phe Ser His Phe Ala Leu Leu Ala Asn Leu 75 gcg gaa gac ctc tac gat gaa gag ctt cgt gaa cag gct ctc gat gca 403 Ala Glu Asp Leu Tyr Asp Glu Glu Leu Arg Glu Gln Ala Leu Asp Ala ggc gac acc cct ccg gac agc act ctt gat gcc acc tgg ctg aaa ctc 451 Gly Asp Thr Pro Pro Asp Ser Thr Leu Asp Ala Thr Trp Leu Lys Leu 110 aat gag ggc aat gtt ggc gca gaa gct gtg gcc gat gtg ctg cgc aat 499

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							aag Lys									595
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							gtc Val									883
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							act Thr									1219

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	_	_	_		-	_	cta Leu 605	_	-		-		-	-		1939

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atg ttc tgc gta atc acc ggc tct gat gat ctg ctt gat gac aac cca Met Phe Cys Val Ile Thr Gly Ser Asp Asp Leu Leu Asp Asp Asn Pro 855 860 865	2707
ctt ctc gca cgc tct gtc cag cgc cga tac ccc tac ctg ctt cca ctc Leu Leu Ala Arg Ser Val Gln Arg Arg Tyr Pro Tyr Leu Leu Pro Leu 870 875 880 885	2755
aac gtg atc cag gta gag atg atg cga cgc tac cga aaa ggc gac caa Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Lys Gly Asp Gln 890 895 900	2803
agc gag caa gtg tcc cgc aac att cag ctg acc atg aac ggt ctt tcc Ser Glu Gln Val Ser Arg Asn Ile Gln Leu Thr Met Asn Gly Leu Ser 905 910 915	2851
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Gln Ala Leu Asp Ala Gly Asp Thr Pro Pro Asp Ser Thr Leu Asp Ala

105

Thr Trp Leu Lys Leu Asn Glu Gly Asn Val Gly Ala Glu Ala Val Ala 115

Asp Val Leu Arg Asn Ala Glu Val Ala Pro Val Leu Thr Ala His Pro 135

Thr Glu Thr Arg Arg Arg Thr Val Phe Asp Ala Gln Lys Trp Ile Thr 145 150

Thr His Met Arg Glu Arg His Ala Leu Gln Ser Ala Glu Pro Thr Ala 170

Arg Thr Gln Ser Lys Leu Asp Glu Ile Glu Lys Asn Ile Arg Arg Arg

190 180 185 Ile Thr Ile Leu Trp Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg 200 Ile Glu Asp Glu Ile Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu 215 Leu Glu Glu Ile Pro Arg Ile Asn Arg Asp Val Ala Val Glu Leu Arg Glu Arg Phe Gly Glu Gly Val Pro Leu Lys Pro Val Val Lys Pro Gly Ser Trp Ile Gly Gly Asp His Asp Gly Asn Pro Tyr Val Thr Ala Glu Thr Val Glu Tyr Ser Thr His Arg Ala Ala Glu Thr Val Leu Lys Tyr Tyr Ala Arg Gln Leu His Ser Leu Glu His Glu Leu Ser Leu Ser Asp 295 Arg Met Asn Lys Val Thr Pro Gln Leu Leu Ala Leu Ala Asp Ala Gly 310 315 His Asn Asp Val Pro Ser Arg Val Asp Glu Pro Tyr Arg Arg Ala Val His Gly Val Arg Gly Arg Ile Leu Ala Thr Thr Ala Glu Leu Ile Gly Glu Asp Ala Val Glu Gly Val Trp Phe Lys Val Phe Thr Pro Tyr Ala Ser Pro Glu Glu Phe Leu Asn Asp Ala Leu Thr Ile Asp His Ser Leu 375 Arg Glu Ser Lys Asp Val Leu Ile Ala Asp Asp Arg Leu Ser Val Leu 395 Ile Ser Ala Ile Glu Ser Phe Gly Phe Asn Leu Tyr Ala Leu Asp Leu Arg Gln Asn Ser Glu Ser Tyr Glu Asp Val Leu Thr Glu Leu Phe Glu Arg Ala Gln Val Thr Ala Asn Tyr Arg Glu Leu Ser Glu Ala Glu Lys Leu Glu Val Leu Leu Lys Glu Leu Arg Ser Pro Arg Pro Leu Ile Pro 455 His Gly Ser Asp Glu Tyr Ser Glu Val Thr Asp Arg Glu Leu Gly Ile 470 475 Phe Arg Thr Ala Ser Glu Ala Val Lys Lys Phe Gly Pro Arg Met Val 485 Pro His Cys Ile Ile Ser Met Ala Ser Ser Val Thr Asp Val Leu Glu 500 505

Pro Met Val Leu Lys Glu Phe Gly Leu Ile Ala Ala Asn Gly Asp 515 520 Asn Pro Arg Gly Thr Val Asp Val Ile Pro Leu Phe Glu Thr Ile Glu 535 Asp Leu Gln Ala Gly Ala Gly Ile Leu Asp Glu Leu Trp Lys Ile Asp 545 550 555 Leu Tyr Arg Asn Tyr Leu Leu Gln Arg Asp Asn Val Gln Glu Val Met 565 570 Leu Gly Tyr Ser Asp Ser Asn Lys Asp Gly Gly Tyr Phe Ser Ala Asn Trp Ala Leu Tyr Asp Ala Glu Leu Gln Leu Val Glu Leu Cys Arg Ser Ala Gly Val Lys Leu Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly 615 Arg Gly Gly Pro Ser Tyr Asp Ala Ile Leu Ala Gln Pro Arg Gly 635 Ala Val Gln Gly Ser Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly Asn Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala Leu 665 Val Ser Ala Thr Leu Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr 680 Asp His Gln Arg Ala Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser Leu Lys Lys Tyr Ala Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp 715 Tyr Phe Thr Gln Ser Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile 730 Gly Ser Arg Pro Ser Ser Arg Lys Gln Thr Ser Ser Val Glu Asp Leu 745 Arg Ala Ile Pro Trp Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe Gly Val Gly Thr Ala Leu Glu Gln Trp Ile Gly Glu Gly Glu Gln Ala Thr Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn Glu 795 Ser Trp Pro Phe Phe Thr Ser Val Leu Asp Asn Met Ala Gln Val Met 805 810

Ser Lys Ala Glu Leu Arg Leu Ala Lys Leu Tyr Ala Asp Leu Ile Pro

825

7

830

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Asp Thr Glu Val Ala Glu Arg Val Tyr Ser Val Ile Arg Glu Glu Tyr Phe Leu Thr Lys Lys Met Phe Cys Val Ile Thr Gly Ser Asp Asp Leu 855 Leu Asp Asp Asn Pro Leu Leu Ala Arg Ser Val Gln Arg Arg Tyr Pro 875 Tyr Leu Leu Pro Leu Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr 885 890 895 Arg Lys Gly Asp Gln Ser Glu Gln Val Ser Arg Asn Ile Gln Leu Thr 900 Met Asn Gly Leu Ser Thr Ala Leu Arg Asn Ser Gly <210> 111 <211> 939 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(916) <223> RXN02326 <400> 111 ccaggcggac agttgtccaa cctgcgtgca caggccaccg cactgggcct tgcggatcgt 60 ttcgaactca tcgaagacaa ctacgcaagc cgttaatgag atg ctg gga cgc cca 115 Met Leu Gly Arg Pro 1 ace aag gte ace cca tee tee aag gtt gtt gge gae ete gea ete cae 163 Thr Lys Val Thr Pro Ser Ser Lys Val Gly Asp Leu Ala Leu His 10 ctc gtt ggt gcg ggt gtg gat cca gca gac ttt gct gcc gat cca caa 211 Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe Ala Ala Asp Pro Gln aag tac gac atc cca gac tct gtc atc gcg ttc ctg cgc ggc gag ctt 259 Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe Leu Arg Gly Glu Leu 40 ggt aac cct cca ggt ggc tgg cca gag cca ctg cgc acc cgc gca ctg 307 Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu Arg Thr Arg Ala Leu gaa ggc cgc tcc gaa ggc aag gca cct ctg acg gaa gtt cct gag gaa 355 Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr Glu Val Pro Glu Glu gag cag gcg cac ctc gac gct gat gat tcc aag gaa cgt cgc aat agc 403 Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys Glu Arg Arg Asn Ser 95 ctc aac cgc ctg ctg ttc ccg aag cca acc gaa gag ttc ctc gag cac 451

Leu As	sn Arg	Leu 105	Leu	Phe	Pro	Lys	Pro 110	Thr	Glu	Glu	Phe	Leu 115	Glu	His	
	gc cgc rg Arg 120														499
Tyr G	gc ctg ly Leu 35														547
_	cc cca nr Pro	_		_	_	_	_						-	-	595
	gt atg Ly Met	_		_		_		-			_		_		643
	gt gtg cg Val														691
	ca gat la Asp 200														739
	c acc al Thr 15														787
	c gca al Ala														835
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-	aa ggt Lu Gly		Asp	_		_	-	-		taaa	acctt	tc t	gtaa	aaagc	936
ccc															939
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Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu 50 55 60

Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr 65 70 75 80

Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys
85 90 95

Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu 100 105 110

Glu Phe Leu Glu His Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp 115 120 125

Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile 130 135 140

Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile 145 150 155 160

Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn 165 170 175

Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val 180 185 190

Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala 195 200 205

Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu 210 215 220

Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu 225 230 235 240

Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val 245 250 255

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1 acc aag gtc acc cca tcc tcc aag gtt gtt ggc gac ctc gca ctc cac 163 Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly Asp Leu Ala Leu His 10 ctc gtt ggt gcg ggt gtg gat cca gca gac ttt gct gcc gat cca caa 211 Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe Ala Ala Asp Pro Gln aag tac gac atc cca gac tct gtc atc gcg ttc ctg cgc ggc gag ctt 259 Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe Leu Arg Gly Glu Leu 40 ggt aac cct cca ggt ggc tgg cca gag cca ctg cgc acc cgc gca ctg 307 Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu Arg Thr Arg Ala Leu gaa ggc cgc tcc gaa ggc aag gca cct ctg acg gaa gtt cct gag gaa 355 Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr Glu Val Pro Glu Glu gag cag gcg cac ctc gac gct gat gat tcc aag gaa cgt cgc aat agc 403 Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys Glu Arg Arg Asn Ser ctc aac cgc ctg ctg ttc ccg aag cca acc gaa gag ttc ctc gag cac 451 Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu Glu Phe Leu Glu His 105 110 cgt cgc cgc ttc ggc aac acc tct gcg ctg gat gat cgt gaa ttc ttc 499 Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp Asp Arg Glu Phe Phe 120 tac ggc ctg gtc gaa ggc cgc gag act ttg atc cgc ctg cca gat gtg 547 Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile Arg Leu Pro Asp Val 135 140 cgc acc cca ctg ctt gtt cgc ctg gat gcg atc tct gag cca gac gat 595 Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile Ser Glu Pro Asp Asp aag ggt atg cgc aat gtt gtg gcc aac gtc aac ggc cag atc cgc cca 643 Lys Gly Met Arg Asn Val Val Ala Asn Val Asn Gly Gln Ile Arg Pro 170 atg cgt gtg cgt gac cgc tcc gtt gag tct gtc acc gca acc gca gaa 691 Met Arg Val Arg Asp Arg Ser Val Glu Ser Val Thr Ala Thr Ala Glu 190 aag gca gat too too aac aag ggo cat gtt gct gca cca tto got ggt 739 Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala Ala Pro Phe Ala Gly 205 gtt gtc acc gtg act gtt gct gaa ggt gat gag gtc aag gct gga gat 787 Val Val Thr Val Thr Val Ala Glu Gly Asp Glu Val Lys Ala Gly Asp 220 gca gtc gca atc atc gag gct atg aag atg gaa gca aca atc act gct 835 Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu Ala Thr Ile Thr Ala 240 235

tct gtt gac ggc aaa atc gat cgc gtt gtg gtt cct gct gca acg aag \$883\$ Ser Val Asp Gly Lys Ile Asp Arg Val Val Val Pro Ala Ala Thr Lys \$250\$ \$255\$ \$260\$

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939

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Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe 35 40 45

Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu 50 55 60

Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr 65 70 75 80

Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys 85 90 95

Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu 100 105 110

Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp 115 120 125

Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile 130 135 140

Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile 145 150 155 160

Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn 165 170 175

Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val 180 185 190

Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala 195 200 205

Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu 210 215 220

Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu

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Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val 255

Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser 260

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														acc Thr		691
														caa Gln		739
	_	-	-	-			_							cac His		787
		_			_		_		_	-	_			cac His		835
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		_	_		_		_		_					gga Gly		931
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caa								•								1083

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Met 65	Leu	Leu	Arg	Gly	Arg 70	Asn	Thr	Val	Gly	Tyr 75	Thr	Pro	Tyr	Pro	Asp 80
Ser	Val	Cys	Arg	Ala 85	Phe	Val	Lys	Glu	Ala 90	Ala	Ser	Ser	Gly	Val 95	Asp
Ile	Phe	Arg	Ile 100	Phe	Asp	Ala	Leu	Asn 105	Asp	Val	Ser	Gln	Met 110	Arg	Pro
Ala	Ile	Asp 115	Ala	Val	Leu	Glu	Thr 120	Asn	Thr	Ala	Val	Ala 125	Glu	Val	Ala
Met	Ala 130	Tyr	Ser	Gly	Asp	Leu 135	Ser	Asp	Pro	Asn	Glu 140	Lys	Leu	Tyr	Thr
Leu 145	Asp	Tyr	Tyr	Leu	Lys 150	Met	Ala	Glu	Glu	Ile 155	Val	Lys	Ser	Gly	Ala 160
His	Ile	Leu	Ala	Ile 165	Lys	Asp	Met	Ala	Gly 170	Leu	Leu	Arg	Pro	Ala 175	Ala
Val	Thr	Lys	Leu 180	Val	Thr	Ala	Leu	Arg 185	Arg	Glu	Phe	Asp	Leu 190	Pro	Val
His	Val	His 195	Thr	His	Asp	Thr	Ala 200	Gly	Gly	Gln	Leu	Ala 205	Thr	Tyr	Phe
Ala	Ala 210	Ala	Gln	Ala	Gly	Ala 215	Asp	Ala	Val	Asp	Gly 220	Ala	Ser	Gly	Thr
Thr 225	Val	Trp	His	His	Leu 230	Pro	Ser	His	Pro	Leu 235	Ser	Ala	Ile	Val	Ala 240
Ala	Phe	Ala	His	Thr 245	_	Arg	Asp	Thr	Gly 250		Ser	Leu	Glu	Ala 255	Val
Ser	Asp	Leu	Glu 260	Pro	Tyr	Trp	Glu	Ala 265	Val	Arg	Gly	Leu	Tyr 270	Leu	Pro
Phe	Glu	Ser 275	Gly	Thr	Pro	Gly	Pro 280	Thr	Gly	Arg	Val	Tyr 285	Arg	His	Glu
Ile	Pro 290	Gly	Gly	Gln	Leu	Ser 295	Asn	Leu	Arg	Ala	Gln 300	Ala	Thr	Ala	Leu
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                                             Leu Leu Ala Thr Arg
gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc gtc gca aag ctg
                                                                   163
Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala Val Ala Lys Leu
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                                                                   211
act cct gag ctt ttg tcc gtg gag gcc tgg ggc gcg acc tac gat
Thr Pro Glu Leu Ser Val Glu Ala Trp Gly Gly Ala Thr Tyr Asp
gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac agg ctc gac gag
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Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp Arg Leu Asp Glu
ctg cgc gag gcg atg ccg aat gta aac att cag atg ctg ctt cgc ggc
                                                                   307
Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met Leu Leu Arg Gly
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                         60
cgc aac acc gtg gga tac acc ccg tac cca gac tcc gtc tgc cgc gcg
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Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser Val Cys Arg Ala
                                                                   403
ttt gtt aag gaa gct gcc agc tcc ggc gtg gac atc ttc cgc atc ttc
Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile Phe Arg Ile Phe
gac gcg ctt aac gac gtc tcc cag atg cgt cca gca atc gac gca gtc
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Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala Ile Asp Ala Val
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Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met Ala Tyr Ser Gly
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Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu
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Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala His Ile Leu Ala Ile
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aag gat atg gct ggt ctg ctt cgc cca gct gcg gta acc aag ctg gtc
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Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val Thr Lys Leu Val
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ggt gca gat gct gtt gac ggt gct tcc ggc acc act gtc tgg cac cac Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr Thr Val Trp His His 215 220 225	787
ctc cca agc cat ccc ttg tct gcc att gtt gct gca ttc gcg cac acc Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala Ala Phe Ala His Thr 230 235 240 245	835
cgt cgc gat acc ggt ttg agc ctc gag gct gtt tct gac ctc gag ccg Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp Leu Glu Pro 250 255 260	883
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Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala 115 120 125°

Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr 130 140

Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala 145 150 155 160

His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala 165 170 175

Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val 180 185 190

His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe 195 200 205

Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr 210 215 220

Thr Val Trp His His Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala 225 230 235 240

Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val 245 250 255

Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro 260 265 270

Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu 275 280 285

Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu 290 295 300

Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ser Arg 305 310 315 320

<210> 119

<211> 1719

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1696)

<223> RXN02328

<400> 119

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gtttgattgg gggaatcggg ggttacgata ctaggacgca gtg act gct atc acc

											Val 1	Thr	Ala	Ile	Thr 5	
				_	_	aaa Lys							_			163
			_			gca Ala			_		_	_	-		_	211
						gct Ala										259
_	_	-	_			ccc Pro 60	-	-	-							307
						gtc Val										355
						gat Asp										403
	_	_	_			ccg Pro										451
						gcg Ala										499
						ctc Leu 140										547
-						ctg Leu										595
						gtt Val										643
						gcc Ala										691
_	_			_		ctt Leu	_			-			-			739
						ggc Gly 220										787
				_		att Ile	_		_				_			835

230	235	240		245
gga gaa gtt gta c Gly Glu Val Val H 2				-
cac caa aaa gtt g His Gln Lys Val V 265				-
ctg cgt gat cgc a Leu Arg Asp Arg I 280		Ala Val Lys Phe		
ggt tac cag ggc g Gly Tyr Gln Gly A 295			l Asp Glu Lys	
aac cac gtc ttc a Asn His Val Phe I 310	_	-		
gtg act gaa gaa g Val Thr Glu Glu V 3				_
ttg gct gct ggt g Leu Ala Ala Gly A 345			•	-
atc aag acc cac g Ile Lys Thr His G 360		Gln Cys Arg Ile		_
cca aac aac ggc t Pro Asn Asn Gly P 375			e Thr Ala Tyr	-
tca cca ggc gga g Ser Pro Gly Gly A 390				
ggc gaa atc acc g Gly Glu Ile Thr A 4				
cgt ggt tcc gac t Arg Gly Ser Asp P 425	_	=		_
gct gag ttc acc g Ala Glu Phe Thr V 440		Ala Thr Asn Ile		
gcg ttg ctg cgg g Ala Leu Leu Arg G 455			g Ile Ala Thr	
ttc att gcc gat c Phe Ile Ala Asp H 470	_			=

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gag cag gga Glu Gln Gly												
cct cat ggt Pro His Gly				l Ala Ala			Lys					
cct aac atc Pro Asn Ile 520		-	-		/ Ser		_					
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Leu Val Ser	Thr His 20	Thr Ser	Ser Thi		Ala :	Phe Lys 30	-	Ile				
Leu Val Ala 35	Asn Arg	Gly Glu	Ile Ala	a Val Aro	, Ala	Phe Arg 45	, Ala	Ala				
Leu Glu Thr 50	Gly Ala	Ala Thr 55	Val Ala	a Ile Tyı	Pro 2	Arg Glu	ı Asp	Arg				
Gly Ser Phe 65	His Arg	Ser Phe 70	Ala Sei	Glu Ala 75		Arg Ile	e Gly	Thr 80				
Glu Gly Ser	Pro Val 85	Lys Ala	Tyr Le	a Asp Ile 90	e Asp (Glu Ile	lle 95	Gly				
Ala Ala Lys	Lys Val 100	Lys Ala	Asp Ala	_	Pro (Gly Tyr 110	_	Phe				
Leu Ser Glu 115	Asn Ala	Gln Leu	Ala Aro	g Glu Cys		Glu Asr 125	Gly	Ile				
Thr Phe Ile 130	Gly Pro	Thr Pro 135	Glu Val	Leu Asp	Leu 1	Thr Gly	Asp	Lys				
Ser Arg Ala 145	Val Thr	Ala Ala 150	Lys Lys	Ala Gly 155		Pro Val	Leu	Ala 160				
Glu Ser Thr	Pro Ser 165	Lys Asn	Ile Asp	Glu Ile 170	· Val 1	Lys Ser	Ala 175	Glu				
Gly Gln Thr	Tyr Pro 180	Ile Phe	Val Lys		. Ala (Gly Gly 190	-	Gly				
Arg Gly Met 195	Arg Phe	Val Ala	Ser Pro 200	Asp Glu		Arg Lys 205	Leu	Ala				

Thr Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val 210 215 220

Tyr Val Glu Arg Ala Val Ile Asn Pro Gln His Ile Glu Val Gln Ile 225 230 235 240

Leu Gly Asp His Thr Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys 245 250 255

Ser Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln 260 265 270

His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys 275 280 285

Phe Cys Arg Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu 290 295 300

Val Asp Glu Lys Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile 305 310 315 320

Gln Val Glu His Thr Val Thr Glu Glu Val Thr Glu Val Asp Leu Val
325 330 335

Lys Ala Gln Met Arg Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly 340 345 350

Leu Thr Gln Asp Lys Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg 355 360 365

Ile Thr Thr Glu Asp Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr 370 375 380

Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly 385 390 395 400

Ala Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu 405 410 415

Val Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg 420 425 430

Ala Gln Arg Ala Leu Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn 435 440 445

Ile Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys
450 455 460

Arg Ile Ala Thr Gly Phe Ile Ala Asp His Pro His Leu Leu Gln Ala 465 470 475 480

Pro Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp 485 490 495

Val Thr Val Asn Lys Pro His Gly Val Arg Pro Lys Asp Val Ala Ala 500 505 510

Pro Ile Asp Lys Leu Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly 515 520 525

Ser Arg Asp Arg

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<222	L> CI 2> (:	OS l) RXA02		3)												
gct		gaa	_		cgc Arg				_				-	_		48
		-		_	gaa Glu				_	-			_		_	96
_	_			_	gga Gly				-		-			_		144
					gaa Glu											192
					acc Thr 70											240
					cca Pro											288
					aaa Lys											336
	-	-	-	_	ggt Gly				-		_	_		_	_	384
					cgc Arg											432
_		_			gat Asp 150			_		_	_	_	_			480
					gaa Glu											528
_	-				gaa Glu	_	_	_		_	_	_	_			576

					gcg Ala											624
					gat Asp											672
					gtg Val 230											720
_			_	_	aac Asn		_		_	-						768
					gtg Val											816
-		_		_	aag Lys	-	_		_			_	_		_	864
			_	-	ctg Leu	_	_	_			_	_	_			912
			-		gat Asp 310								_			960
		_		-	cgt Arg		_		_	_	_				_	1008
		_			gac Asp		_	_			_		_	_		1056
	_		_		gct Ala	_	_	_	_	_	_		_	-		1104
					gtt Val											1152
					ttc Phe 390											1200
					ctc Leu											1248
					tac Tyr											1296

ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg cct aac 1344 Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu Pro Asn 435 440 ate aag gat etg eea etg eea ege ggt tee egt gae ege tgaageaget 1393 Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg 450 455 tggcccagcc gcg 1406 <210> 122 <211> 461 <212> PRT <213> Corynebacterium glutamicum <400> 122 Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg Phe Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg Glu Ala 135 Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala Val Ile Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln 185 Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg 200 Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile Gly Tyr 210 215 Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly Asn His

235

260 265 270

Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Lys 275 280 285

Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Asn 290 295 300

Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg Ser Pro 305 310 315 320

Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly Glu 325 330 335

Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly 340 345 350

Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu Ala Glu 355 360 365

Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg Ala Leu 370 380

Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly Phe Ile 385 390 395 400

Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp Glu Gln 405 410 415

Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His
420 425 430

Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu Pro Asn 435 440 445

Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg 450 455 460

<210> 123

<211> 1347

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1324)

<223> RXN01048

<400> 123

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gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 119 Met Thr Ile Asp Leu 1 5

					aac Asn											163
					tcc Ser		_			_	_		_	-	_	211
					gct Ala					_	-	-	-	_	_	259
					cca Pro											307
					att Ile 75											355
					gcc Ala											403
					gct Ala											451
_		_	_	-	gct Ala	_					-	_				499
					aac Asn	_		-			_		-	-		547
					ctc Leu 155											595
					acc Thr	_		_			-		-	_		643
					gat Asp											691
tcc Ser	ggc Gly	gca Ala 200	ggc Gly	gca Ala	gcg Ala	ggc Gly	gtt Val 205	gca Ala	gct Ala	gta Val	gat Asp	atg Met 210	ctg Leu	acc Thr	aac Asn	739
					atc Ile											787
					ctt Leu 235											835
acc	aac	cct	cgt	ggc	atc	agc	ggt	ggc	atc	aat	gag	gct	ttc	acc	ggc	883

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Thr	Asn	Pro	Arg	Gly 250	Ile	Ser	Gly	Gly	Ile 255	Asn	Glu	Ala	Phe	Thr 260	Gly	
						gtg Val										931
						gag Glu										979
				_		gag Glu 300	_		_	_			_		_	1027
			_		_	ctg Leu			_					_		1075
					_	ggc Gly	_		_	_	_	_	-	_		1123
			_	_		gcc Ala	_	_			_	_		_	_	1171
						gcc Ala										1219
	_			_		agg Arg 380	_	-			_	_		_	_	1267
	_				-	ctt Leu		-	-				-			1315
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<210> 124

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 124

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu 1 5 10 15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg $20 \hspace{1cm} 25 \hspace{1cm} 30$

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val\$35\$ 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr 50 55 60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala 65 70 75 80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met 85 90 95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile 100 105 110

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile 115 120 125

Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser 130 135 140

Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp 145 150 155 160

Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu 165 170 175

Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp 180 185 190

Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val 195 200 205

Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser 210 215 220

Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala 225 230 235 240

Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn 245 250 255

Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn 260 265 270

Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe 275 280 285

Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys 290 295 300

Tyr Gly Ala Ile Val Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile 305 310 315 320

Asn Asn Val Leu Ala Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala 325 330 335

Lys Ala Lys Lys Ile Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln 340 345 350

Ser Gln Thr Ser Gln Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu 355 360 365

Pro Pro Trp Ile Pro Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg 370 375 380 BGI-126CP - 188 -

Pro Ser Pro Lys Arg Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser 385 390 395 400

Leu Pro Val Glu Ala Pro Ile Phe 405

<210> 125

<211> 311

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(288)

<223> FRXA01048

<400> 125

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atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag ctg agg acc $$ 144 Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr $$ 35 $$ 40 $$ 45

tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc 192 Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro 50 55 60

caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt 240 Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu 65 70 75 80

aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt 288 Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe 85 90 95

taagagcaaa cttgaggccc aca 311

<210> 126

<211> 96

<212> PRT

<213> Corynebacterium glutamicum

<400> 126

Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
1 5 10 15

Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu 20 25 30

Met Lys Leu Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr 35 40 45

Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro

50 55 60

Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu 65 70 75 80

Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe 85 90 95

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125

						ttg Leu 140						547
				-		atc Ile	 _		_		_	595
						gct Ala						643
						cgc Arg						691
						ggc Gly						739
						gtg Val 220						787
						tcc Ser						835
						agc Ser						883
						gtg Val						931
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						gag Glu 300						1027
						acc Thr						1063
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<211> 321

<212> PRT

<213> Corynebacterium glutamicum

<400> 128

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu 1 5 10 15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg $20 \hspace{1cm} 25 \hspace{1cm} 30$

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val $$ $$ 35 $$ 40 $$ 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr 50 55 60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala 65 70 75 80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met 85 90 95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile 100 105 110

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile 115 120 125

Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser 130 135 140

Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp 145 150 155 160

Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu 165 170 · 175

Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp 180 185 190

Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val 195 200 205

Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser 210 215 220

Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala 225 230 235 240

Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn 245 250 255

Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn 260 265 270

Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe 275 280 285

Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys 290 295 300

Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg 305 310 315 320

Ser

<210> 129

<211> 1065

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1042)

<223> RXA02694

<400> 129

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				1				5	

ggt	aac	aag	att	gtc	ctc	att	ggc	gca	gga	gat	gtt	gga	gtt	gca	tac	163
Gly	Asn	Lys	Ile	Val	Leu	Ile	Gly	Ala	Gly	Asp	Val	Gly	Val	Ala	Tyr	
				10					15					20		

gca	tac	gca	ctg	atc	aac	cag	ggc	atg	gca	gat	cac	ctt	gcg	atc	atc	211
Ala	Tyr	Ala	Leu	Ile	Asn	Gln	Gly	Met	Ala	Asp	His	Leu	Ala	Ile	Ile	
			25					30					35			

gac	atc	gat	gaa	aag	aaa	ctc	gaa	ggc	aac	gtc	atg	gac	tta	aac	cat	259
Asp	Ile	Asp	Glu	Lys	Lys	Leu	Glu	Gly	Asn	Val	Met	Asp	Leu	Asn	His	
		40					4.5					50				

ggt	gtt	gtg	tgg	gcc	gat	tcc	cgc	acc	cgc	gtc	acc	aag	ggc	acc	tac	307
Gly	Val	Val	Trp	Ala	Asp	Ser	Arg	Thr	Arg	Val	Thr	Lys	Gly	Thr	Tyr	
	55					60					65					

gct	gac	tgc	gaa	gac	gca	gcc	atg	gtt	gtc	att	tgt	gcc	ggc	gca	gcc	355
Ala	Asp	Cys	Glu	Asp	Ala	Ala	Met	Val	Val	Ile	Cys	Ala	Gly	Ala	Ala	
70					75					80					85	

caa	aag	cca	aac	gag	acc	cac	ctc	caq	cta	ata	gac	aaa	aac	atc	aaq	403
	_					_		_	_		_			_		
GIN	ьys	Pro	GLY	Glu	Thr	Arg	Leu	GIn	Leu	٧aı	Asp	Lys	Asn	٧al	Lys	
				90					0.5			-		100	_	

att atg aaa too ato gto ggo gat gto atg gao ago gga tto gao ggo 45:	1
	_
The Met Inc Con The Wel Clar Acc Wel Met Acc Con Clar Die Acc Cl	
Ile Met Lys Ser Ile Val Gly Asp Val Met Asp Ser Gly Phe Asp Gly	
105 110 115	

		 	aac Asn		-	_	_			_	 499
	120	 	 	125			 	130	-] -		

tgg	aaa	ttc	tcc	ggc	ttg	gaa	tgg	aac	cgc	gtg	atc	ggc	tcc	gga	act	547
Trp	Lys	Phe	Ser	Gly	Leu	Glu	Trp	Asn	Arg	Val	Ile	Gly	Ser	Gly	Thr	
	135					140					145					

gtc	ctg	gac	tcc	gct	cga	ttc	cgc	tac	atg	ctg	ggc	gaa	ctc	tac	gaa	595
Val	Leu	Asp	Ser	Ala	Arg	Phe	Arg	Tyr	Met	Leu	Gly	Glu	Leu	Tyr	Glu	
150					155					160					165	

gtg	gca	cca	agc	tcc	gtc	cac	gcc	tac	atc	atc	ggc	gaa	cac	ggc	gac	643
Val	Ala	Pro	Ser	Ser	Val	His	Ala	Tvr	Ile	Ile	Glv	Glu	His	Glv	Asp	
•				170				-			1				P	
				1/0					.175					180		

act	gaa	ctt	cca	gtc	ctg	tcc	tcc	gcg	acc	atc	gca	ggc	gta	tcg	ctt	69	1
Thr	Ğlu	Len	Pro	Val	Len	Ser	Ser	Δla	Thr	Tle	Ala	Glv	۷al	Ser	I.e.ii		
	υ						UCL	1114				O ± y	v 0.1		Ti C G		
			185					190					195				
			+ 0 0					エンし					エンン				

agc cga atg ctg gac aaa gac cca gag ctt gag ggc cgt cta gag aaa Ser Arg Met Leu Asp Lys Asp Pro Glu Leu Glu Gly Arg Leu Glu Lys 200 205 210	739
att ttc gaa gac acc cgc gac gct gcc tat cac att atc gac gcc aag Ile Phe Glu Asp Thr Arg Asp Ala Ala Tyr His Ile Ile Asp Ala Lys 215 220 225	787
ggc tcc act tcc tac ggc atc ggc atg ggt ctt gct cgc atc acc cgc Gly Ser Thr Ser Tyr Gly Ile Gly Met Gly Leu Ala Arg Ile Thr Arg 230 235 240 245	835
gca atc cta cag aac caa gac gtt gca gtc cca gtc tct gca ctg ctc Ala Ile Leu Gln Asn Gln Asp Val Ala Val Pro Val Ser Ala Leu Leu 250 255 260	883
cac ggt gaa tac ggt gag gaa gac atc tac atc ggc acc cca gct gtg His Gly Glu Tyr Gly Glu Glu Asp Ile Tyr Ile Gly Thr Pro Ala Val 265 270 275	931
gtg aac cgc cga ggc atc cgc cgc gtt gtc gaa cta gaa atc acc gac Val Asn Arg Arg Gly Ile Arg Arg Val Val Glu Leu Glu Ile Thr Asp 280 285 290	979
cac gag atg gaa cgc ttc aag cat tcc gca aat acc ctg cgc gaa att His Glu Met Glu Arg Phe Lys His Ser Ala Asn Thr Leu Arg Glu Ile 295 300 305	1027
cag aag cag ttc ttc taaatctttg gcgcctagtt ggc Gln Lys Gln Phe Phe	1065
310	
<pre>310 <210> 130 <211> 314 <212> PRT <213> Corynebacterium glutamicum</pre>	
<210> 130 <211> 314 <212> PRT	
<210> 130 <211> 314 <212> PRT <213> Corynebacterium glutamicum <400> 130 Met Lys Glu Thr Val Gly Asn Lys Ile Val Leu Ile Gly Ala Gly Asp	
<pre> <210> 130 <211> 314 <212> PRT <213> Corynebacterium glutamicum <400> 130 Met Lys Glu Thr Val Gly Asn Lys Ile Val Leu Ile Gly Ala Gly Asp</pre>	
<pre> <210> 130 <211> 314 <212> PRT <213> Corynebacterium glutamicum <400> 130 Met Lys Glu Thr Val Gly Asn Lys Ile Val Leu Ile Gly Ala Gly Asp</pre>	
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Ser Gly Phe Asp Gly Ile Phe Leu Val Ala Ser Asn Pro Val Asp Ile 120 Leu Thr Tyr Ala Val Trp Lys Phe Ser Gly Leu Glu Trp Asn Arg Val 130 135 Ile Gly Ser Gly Thr Val Leu Asp Ser Ala Arg Phe Arg Tyr Met Leu 155 Gly Glu Leu Tyr Glu Val Ala Pro Ser Ser Val His Ala Tyr Ile Ile Gly Glu His Gly Asp Thr Glu Leu Pro Val Leu Ser Ser Ala Thr Ile 185 Ala Gly Val Ser Leu Ser Arg Met Leu Asp Lys Asp Pro Glu Leu Glu Gly Arg Leu Glu Lys Ile Phe Glu Asp Thr Arg Asp Ala Ala Tyr His 215 Ile Ile Asp Ala Lys Gly Ser Thr Ser Tyr Gly Ile Gly Met Gly Leu 235 Ala Arg Ile Thr Arg Ala Ile Leu Gln Asn Gln Asp Val Ala Val Pro Val Ser Ala Leu Leu His Gly Glu Tyr Gly Glu Glu Asp Ile Tyr Ile Gly Thr Pro Ala Val Val Asn Arg Arg Gly Ile Arg Arg Val Val Glu Leu Glu Ile Thr Asp His Glu Met Glu Arg Phe Lys His Ser Ala Asn 295 300 Thr Leu Arg Glu Ile Gln Lys Gln Phe Phe 310 <210> 131 <211> 2967 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(2944) <223> RXN00296 <400> 131 tttttgttgg catgtctgac attatcgcac aattcaccac agtaaccggt aacatgttac 60 tcaaagcccg cttggatcga atttcacaaa aggacccacc atg act cac acc atc Met Thr His Thr Ile 1 aaa ttc aac aga ctc gac cca gaa gta ttt agc cag cat tct cgc gcg 163 Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser Gln His Ser Arg Ala

15

20

_	_	_	_	-	atg Met			_	-	-				_	_	211
			_	_	gtc Val		-	-	-	_	-		-			259
					gcc Ala											307
_	_		_		gga Gly 75		_	_	_	_						355
_		_			gat Asp	-		_				_			_	403
					caa Gln											451
					gca Ala											499
					tcc Ser											547
					cac His 155											595
		_	-	-	ctc Leu	-			_		_	_	_			643
					gat Asp											691
			_		cag Gln	-			_		-	_		_		739
	_			_	ggc Gly			_				-		-	_	787
_		-	_		ggc Gly 235											835
_	_		_	-	gtt Val									_	-	883
ctg	gct	ttc	gac	acg	gtt	ttt	gac	gcc	gcc	cga	gca	gcc	gcc	aaa	ttg	931

Leu	Ala	Phe	Asp 265	Thr	Val	Phe	Asp	Ala 270	Ala	Arg	Ala	Ala	Ala 275	Lys	Leu	
	ctg Leu															979
	gcg Ala 295															1027
	gga Gly		_				_	_				-		_		1075
	gga Gly	_	_			_	-	-								1123
_	acc Thr	_	_	_			_			_						1171
_	atg Met		_	_		_		_	-		_				_	1219
	cgc Arg 375															1267
	gtg Val						_	_			_	-				1315
	atg Met															1363
	ggc Gly				Val	Arg	Ile		Phe	Asp	Phe	Ser				1411
	ctg Leu															1459
	tct Ser 455															1507
	tca Ser															1555
	gaa Glu	-		_	_			-		_	_					1603
	gtg Val															1651

	505	510		515	
		-	ccc gta cac as Pro Val His Ly 53	s Phe Ser	
	_		aat cgc tgc gt Asn Arg Cys Va 545		
	_		tgc ccg tcc tt Cys Pro Ser Ph 560		
	_		cgc gcc cgc tt Arg Ala Arg Le 575	•	
			ggc tac cgc ag Gly Tyr Arg Se	, , ,	-
	-	_	tgc aaa gca tg Cys Lys Ala Cy 63	s Ala Ser	-
- ,-		_	tac aaa gcc ga Tyr Lys Ala Gl 625	_	-
		-	atg gcc cat ta Met Ala His Ty 640		
			cat aaa ata co His Lys Ile Pr 655	-	
			gca ctc acc go Ala Leu Thr Al		
			ccg ttg att to Pro Leu Ile Se	er Phe Ala	
			aaa aac tca go Lys Asn Ser Gl 705		
	-		aac ctc gac ac Asn Leu Asp Th 720		-
			ctc ggt tac as Leu Gly Tyr As 735		
		, ,,	acc tgg cat to Thr Trp His Se		

					aaa Lys										2419
		_	_		ggt Gly		_	_		_	_		_	-	2467
					gat Asp 795										2515
				-	gca Ala					-	-			_	2563
	_				cta Leu	-			_		_			-	2611
					cag Gln		_			_	_			-	2659
				-	ctc Leu	_	-	_	_		_		_	_	2707
		_			tgt Cys 875	_		_						_	2755
			-	_	atg Met		_			_	_	-	_		2803
					gca Ala	_				_	_				2851
					gaa Glu										2899
		Val			agc Ser										2944
taa	cgato	cat q	gcaa	caggt	g ct	c									2967

<210> 132

<211> 948

<212> PRT

<213> Corynebacterium glutamicum

<400> 132

Met Thr His Thr Ile Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Gln His Ser Arg Ala Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala 20 25 30

Tyr Ser Ser Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala 35 40 \cdot 45

Glu Pro Glu Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val 50 55 60

Ala Arg Gly Trp Ser Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala 65 70 75 80

Gly Asn Ala Ile Gly Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe
85 90 95

Asn Arg Ile Leu Asp Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu 100 105 110

Pro Gly Val Val Cys Asp Ala Leu Arg Asp Ala Ala Glu Phe Gly 115 120 125

Leu Thr Tyr Gly Pro Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly 130 135 140

Gly Met Val Ala Asn Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly
145 150 155 160

Thr Ala Ala Glu Asn Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly
165 170 175

Arg Glu Val Thr Val Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn 180 185 190

Gln Lys Leu Thr Asp Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys 195 200 205

Glu Leu Gly Arg Phe Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr 210 215 220

Leu Ala His Asp Met Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile 225 230 235 240

Gly Ile Ile Thr Arg Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val 245 250 255

Lys Ala Leu Ala Val Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg 260 265 270

Ala Ala Lys Leu Arg Leu Pro Gly Val Ala Thr Ile Glu Gly Met 275 280 285

Gly Gly Asp Leu Leu Ala Ala Leu Arg Ser Lys Gln Gly Gln Ser Glu 290 295 300

Ala Gly Gln Asn Leu Pro Gly Asn Arg Ile Gly Ile Glu Ala Gly Gly 305 310 315 320

Trp Leu Tyr Cys Glu Thr Gly Ser Asp Thr Leu Gln Ala Ala Val Gln 325 330 335

Ala Ala Glu Glu Val Ala Thr Ala Val Asp Thr Ile Asp Tyr Val Val

340 345 350 Val Ser Glu Pro Ser Glu Met Arg Glu Leu Trp Arg Ile Arg Glu Ser Ser Ala Gly Ile Val Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro 375 Asn Trp Glu Asp Ser Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu 395 Arg Asp Leu Tyr Ala Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro 405 Phe Gly His Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp Phe Ser Thr Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu 435 Ala Ser Thr Leu Val Ala Ser Tyr Gly Gly Ser Leu Ser Gly Glu His Gly Asp Gly Arg Ala Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala Glu Met Arg Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln 490 Arg Ile Phe Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln 505 Gly Leu Arg Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val His Lys Phe Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg 535 Cys Val Gly Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro Ser Phe Gln Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala Arg Leu Leu Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr 585 Arg Ser Glu Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys Ala Cys Ala Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys Ala Glu Phe Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala 635 His Tyr Val Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys 645 Ile Pro Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu 660 665

Thr Ala Pro Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu 675 680 685

Ile Ser Phe Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn 690 695 700

Ser Gly Glu Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu 705 710 715 720

Asp Thr Gly Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly
725 730 735

Tyr Asn Val Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp 740 745 750

His Ser Thr Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr 755 760 765

Ala Lys Val Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly 770 775 780

Leu Glu Pro Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu 785 790 795 800

Ser Asp Asn Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe 805 810 815

Ala Glu Val Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser 820 825 830

Leu Gln Leu Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu 835 840 845

Arg Ser Leu Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu 850 855 860

Gly Val Lys Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly 865 870 875 880

Asn Trp Gly Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly 885 890 895

Glu Arg Glu Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile 900 905 910

Ala Asp Gly Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys 915 920 925

Gln Ala Thr His Leu Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn 930 935 940

Asn Met Ala Gln 945

<210> 133

<211> 2858

<212> DNA

<213> Corynebacterium glutamicum

<220> <221> CDS <222> (1)..(2835) <223> FRXA00296 <400> 133 acc atc aaa ttc aac aga ctc gac cca gaa gta ttt agc cag cat tct Thr Ile Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser Gln His Ser cgc gcg aag ctg cgc acg gat atg aca acc cgt gca gca tat tct tct Arg Ala Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala Tyr Ser Ser gat gca gga att ttt aga cgc gtc cct gca gct gta gct gaa cca gaa 144 Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu 35 aat gtg gaa caa att cgt gat gcc att gct gtt gcg gtg gca cga ggg 192 Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly tgg tet gtt ggg cgc ggt gga gga agc teg gtt get gga aat geg 240 Trp Ser Val Val Gly Arg Gly Gly Ser Ser Val Ala Gly Asn Ala atc ggt gaa ggt ttg atc atc gat acg tca cgc tat ttc aac cgc att 288 Ile Gly Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile 85 tta gat att gat cca gtt gca caa act gca gtt gtg gaa ccc ggt gtg 336 Leu Asp Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val 100 gtg tgt gat gcc ttg cgc gat gca gcc gca gaa ttc gga tta act tac 384 Val Cys Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr 115 120 ggc ccg gat cct tcc acg cat tcc cgg tgc acg atc ggt ggc atg gtt 432 Gly Pro Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val 135 gcc aac aat gcg tgt ggt tca cac tcg gtt gca ttc ggt aca gct gcg 480 Ala Asn Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala gaa aat ctc gtg gat gtc acg ctc atg ctc agc gat ggc cga gaa gtc 528 Glu Asn Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val act gtg aca aaa gat ggc tgc gat gat gct gag atc aat cag aag ctc 576 Thr Val Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu 185 acc gac tta gcg tcc aag aat cag gac ctt att agt aaa gaa ctg ggt 624 Thr Asp Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly 200 cgt ttc cct cgc caa gtg tcg ggc tac ggt ttg cat tat ctt gcc cac 672 Arg Phe Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His 210 215 220

				atg Met 230								720
				aag Lys								768
				gac Asp								816
				ggg Gly								864
				cgc Arg								912
				cgc Arg 310								960
				gac Asp								1008
				gtt Val								1056
				gaa Glu								1104
-	-	_		gct Ala	-		 -	 	_		-	1152
				cca Pro 390								1200
	_	_	_	aag Lys		_	_					1248
				gtc Val								1296
				aaa Lys								1344
				ggt Gly								1392

					ttc Phe 470											1440
-			_	_	ttc Phe	_	_			-		_	_			1488
					gtc Val											1536
_	_	_		_	cgc Arg	_		-		_		_				1584
		-			tcc Ser	_						_	_			1632
					tca Ser 550											1680
					gta Val											_. 1728
		_		_	ggt Gly	_			_	_			_	_	_	1776
					ctt Leu											1824
					aac Asn											1872
					gcc Ala 630											1920
					ctt Leu											1968
					gac Asp											2016
					ggc Gly											2064
-		_	_	-	cgc Arg	_		_	_	_					-	2112
acg	gtg	gtg	ctg	tgg	ccc	gat	tcc	ttc	aac	acc	aac	ctc	gac	acc	gga	2160

Thr 705	Val	Val	Leu	Trp	Pro 710	Asp	Ser	Phe	Asn	Thr 715	Asn	Leu	Asp	Thr	Gly 720	
	gct Ala		_						_	_						2208
	atc Ile															2256
	caa Gln															2304
	aaa Lys 770															2352
	tgc Cys															2400
	gat Asp															2448
	gca Ala													-		2496
	gaa Glu															2544
	gac Asp 850				_	_		_		_	_	_		-		2592
	gaa Glu			Ala		Gly			Gly							2640
	gaa Glu															2688
	ttc Phe															2736
	tcc Ser															2784
	ctt Leu 930															2832
caa Gln	taad	cgato	cat o	gcaad	caggt	g ct	c									2858

<210> 134

<211> 945

<212> PRT

<213> Corynebacterium glutamicum

<400> 134

Thr Ile Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser Gln His Ser 1 5 10 15

Arg Ala Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala Tyr Ser Ser 20 25 30

Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu 35 40 45

Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly
50 55 60

Trp Ser Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala 65 70 75 80

Ile Gly Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile 85 90 95

Leu Asp Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val
100 105 110

Val Cys Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr 115 120 125

Gly Pro Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val 130 135 140

Ala Asn Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala 145 150 155 160

Glu Asn Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val 165 170 175

Thr Val Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu 180 185 190

Thr Asp Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly
195 200 205

Arg Phe Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His 210 215 220

Asp Met Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile 225 230 235 240

Thr Arg Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val Lys Ala Leu 245 250 255

Ala Val Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg Ala Ala Ala 260 265 270

Lys Leu Arg Leu Pro Gly Val Ala Thr Ile Glu Gly Met Gly Gly Asp

275 280 285 Leu Leu Ala Ala Leu Arg Ser Lys Gln Gly Gln Ser Glu Ala Gly Gln 295 Asn Leu Pro Gly Asn Arg Ile Gly Ile Glu Ala Gly Gly Trp Leu Tyr 305 310 Cys Glu Thr Gly Ser Asp Thr Leu Gln Ala Ala Val Gln Ala Ala Glu 330 Glu Val Ala Thr Ala Val Asp Thr Ile Asp Tyr Val Val Val Ser Glu 340 Pro Ser Glu Met Arg Glu Leu Trp Arg Ile Arg Glu Ser Ser Ala Gly 360 Ile Val Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro Asn Trp Glu Asp Ser Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu Arg Asp Leu Tyr Ala Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro Phe Gly His Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp Phe Ser Thr Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu Ala Ser Thr Leu Val Ala Ser Tyr Gly Gly Ser Leu Ser Gly Glu His Gly Asp Gly 455 Arg Ala Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala Glu Met Arg 475 Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln Arg Ile Phe Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln Gly Leu Arg 505 Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val His Lys Phe Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg Cys Val Gly 535 Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro Ser Phe Gln Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala Arg Leu Leu 570 Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr Arg Ser Glu 580 585 Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys Ala Cys Ala 600 595

Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys Ala Glu Phe 615 Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val 635 Met Gly Trp Leu Pro Leu Gly His Val Ala His Lys Ile Pro Leu 645 Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro 665 Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe 675 Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly 715 Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly Tyr Asn Val 730 Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp His Ser Thr Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr Ala Lys Val Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn 795 Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val 810 Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu 825 Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu 840 Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu Gly Val Lys Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly 875 Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu 885 890 Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly 905 Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys Gln Ala Thr

His Leu Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn Asn Met Ala 935 Gln 945 <210> 135 <211> 1383 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1360) <223> RXA01901 <400> 135 gcatgttgcc ttctctctgt gatcgcctcg ttcttcatcc aacgcgtcgc gcaccaagag 60 aactaaaatc taagtaaaac ccctccgaaa ggaaccaccc atg gtg aaa cgt caa 115 Met Val Lys Arg Gln 1 ctg ccc aac ccc gca gaa cta ctc gaa ctc atg aag ttc aaa aag cca 163 Leu Pro Asn Pro Ala Glu Leu Leu Glu Leu Met Lys Phe Lys Lys Pro gag etc aac gge aag aaa ega ege eta gae tee geg etc ace ate tae 211 Glu Leu Asn Gly Lys Lys Arg Arg Leu Asp Ser Ala Leu Thr Ile Tyr 25 gac ctg cgt aaa att gct aaa cga cgc acc cca gct gcc gcg ttc gac 259 Asp Leu Arg Lys Ile Ala Lys Arg Arg Thr Pro Ala Ala Ala Phe Asp 40 307 tac acc gac ggc gca gcc gag gcc gaa ctc tca atc aca cgc gca cgt Tyr Thr Asp Gly Ala Ala Glu Ala Glu Leu Ser Ile Thr Arg Ala Arg gaa gca ttc gaa aac atc gaa ttc cac cca gac atc ctc aag cct gca 355 Glu Ala Phe Glu Asn Ile Glu Phe His Pro Asp Ile Leu Lys Pro Ala gaa cac gta gac acc acc caa atc ctg ggc gga acc tcc tcc atg 403 Glu His Val Asp Thr Thr Gln Ile Leu Gly Gly Thr Ser Ser Met cca ttc ggc atc gca cca acc ggc ttc acc cgc ctc atg cag acc gaa 451 Pro Phe Gly Ile Ala Pro Thr Gly Phe Thr Arg Leu Met Gln Thr Glu 110 ggt gaa atc gca ggt gcc gga gct gca ggc gct gca gga att cct ttc 499 Gly Glu Ile Ala Gly Ala Gly Ala Gly Ala Ala Gly Ile Pro Phe 125 acc ctg tcc acc ctg ggc act acc tcc atc gaa gac gtc aag gcc acc 547 Thr Leu Ser Thr Leu Gly Thr Thr Ser Ile Glu Asp Val Lys Ala Thr 140 aac ccc aac ggc cga aac tgg ttc cag ctc tac gtc atg cgc gac cgc

Asn 150	Pro	Asn	Gly	Arg	Asn 155	Trp	Phe	Gln	Leu	Tyr 160	Val	Met	Arg	Asp	Arg 165	
_						gtc Val	_	_	-	_		_			_	643
	_					gat Asp										691
_		_				tcc Ser		_		_	_					739
			-			cgc Arg 220						-		_		787
						gca Ala				_						835
	-					gcg Ala	-	-						-	-	883
						atg Met										931
-	-		-	-	-	tcc Ser	-				-			-	_	979
						cac His 300			-			-	-	-		1027
_					_	cca Pro	_	_	_	_	_	_			_	1075
			_		_	acc Thr			_			-	_		_	1123
						gct Ala										1171
				_	_	gga Gly		_	_		-	-	_			1219
acc							200	000		2+4	act	ctc	at a	~~+		1067
_	att Ile 375		-	_		Ile 380		_		_	-				_	1267

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Leu	Val	Val 275	Lys	Gly	Val	Gln	Asn 280	Val	Glu	Asp	Ser	Val 285	Lys	Leu	Leu	
Asp	Gln 290	Gly	Val	Asp	Gly	Leu 295	Ile	Leu	Ser	Asn	His 300	Gly	Gly	Arg	Gln	
Leu 305	Asp	Arg	Ala	Pro	Val 310	Pro	Phe	His	Leu	Leu 315	Pro	Gln	Val	Arg	Lys 320	
Glu	Val	Gly	Ser	Glu 325	Pro	Thr	Ile	Met	Ile 330	Asp	Thr	Gly	Ile	Met 335	Asn	
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	acc Thr															163
	ggc Gly															211

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- 213 -

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	atg Met															1075
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	tcg Ser		_	-		-									ggc. Gly	1171
	ggt Gly	_			-	-	_	_	_		_	_				1219
_	ccc Pro 375		_	_		_	_	_	_			_		_	ttc Phe	1267
	cat His		_	-			_			-		_	_		_	1315
-	aag Lys	_		-				_	-						-	1363
	ttc Phe		-	-		_	_	-	_	-		_				1411
	ggc Gly		-	-	_	_		_		-		_	_	_		1459
	atc Ile 455															1507
	aac Asn														gag [.] Glu 485	1555
	aag Lys															1603
	gtc Val			_			_									1651
	cac His															1699

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à

210 215 220 Ser Asn Glu Thr Glu Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser 230 235 Pro Ala Arg Tyr Asn Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly 245 Ser Ala Gly Lys Leu Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro Arg Glu Val His Pro Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His Glu Leu Glu Glu Ile Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu Pro Ile Ser Gly Glu Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu 315 . Lys Tyr Gly Lys Asp Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala Leu Gln Thr Arg Met Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe Ser Lys Ile Pro Gly Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln Ala Met Phe Ser Val Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu 375 Tyr Arg Asn Arg Phe Glu His His Leu Leu Leu Thr Val Ser Glu Ser 395 Gln Lys Ala Ala Ser Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro Glu His Thr Gly Glu Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser Ala Ser Leu Asn Arg Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala Ala Leu Lys Arg Arg His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala Leu Arg Arg Asp Asp Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile 470 475 Asp Asp Gln Leu Glu Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His 485 Val Met His Gln Asp Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala 505 Leu His Asp Arg Ile Gln His Leu Leu Glu Glu Arg Gly Ala Lys Leu 515 Pro Ala Glu His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met 535 540

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                                                                    96
cgc atc cag cac ttg ctg gag gag cac ggc aag aag ctg ccc gcc gag
Arg Ile Gln His Leu Leu Glu Glu His Gly Lys Lys Leu Pro Ala Glu
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cac aac tac ggt cgc atg tac aag ctg ccg gag tcc atg gaa gag cac
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His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met Glu Glu His
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                                                                   192
ttc aag gag ctc gat ccg acg aat acg ttc aac gcc ggt atc ggc ggc
Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly
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Gln Thr Thr Thr Ser His Glu Ala Ile Asp Ala Phe Lys Arg Ile
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                                                                   211
Val Gly Asp Glu His Val Leu Thr Ser Glu Arg Ala Thr Met Pro Phe
age aaa gge tat ega tte gge gga gga eea gte tte gee gtg gtg ege
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Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val Phe Ala Val Arg
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Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu Gln Val Ser Val Asp
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Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn Thr Gly Leu Thr Gly
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Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg Pro Ile Val Ile Ile
teg act cac ege ate gat gag gtg cac etc ate aac gae geg ege gag
                                                                   451
Ser Thr His Arg Ile Asp Glu Val His Leu Ile Asn Asp Ala Arg Glu
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Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His Leu Thr Asp Ala Leu
gcc aag cac cag cgc gag ccg cac tcg gtg atc ggg tcg aca tca atc
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Ala Lys His Gln Arg Glu Pro His Ser Val Ile Gly Ser Thr Ser Ile
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gge gee teg gte ate gge gge ate geg aac aac teg gge gge age cag
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Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn Ser Gly Gly Ser Gln
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Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala Ile Phe Ala Arg Val
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gcg Ala															883
atg Met					_	_				_	_			_	931
acc Thr															979
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tac Tyr 310	_		_	_	_	_	_	-		_				-	1075
acc Thr		_		_	_	_	_			_	_	_	_	-	1123
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att (1219
ctg Leu															1267
gag Glu 390															1315
gag (1363

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						ctg Leu										1555
_	_					cac His			_			-		_	-	1603
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115 120 125

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BGI-126CP - 222 -

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gat cag cag a Asp Gln Gln 1			-		
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gca aag tct t Ala Lys Ser I 150	•	, ,,		•	
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gac cat gtg o Asp His Val V					
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<211> 168

<212> PRT

<213> Corynebacterium glutamicum

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gcg ctt gga gat gca gta gaa gtc cgt tgg gtt gac gga cct aac cgc

Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val Asp Gly Pro Asn Arg

30

25

	_	_		_	_	_	_	_		_	_	ctg Leu 50			_	259
												gcc Ala				307
_		_		_	_				_	_		gtt Val	_			355
												ccg Pro				403
												ctg Leu				451
												gcg Ala 130				499
												ctg Leu				547
_	_	_	_			_	_	_	_		_	gtc Val	_	_	_	595
	_			_	_		_			_		acc Thr	_		_	643
	ggt Gly															649

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<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 152

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Gln Ser Thr Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val

Asp Gly Pro Asn Arg Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp 35 40 45

Ala Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala 50 55 60

Ala Ala Pro Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp 65 70 75 80

Asn Val Asp Ile Pro Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn 85 Ala Pro Thr Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ser Leu 105 Leu Leu Ser Thr Ala Arg Gln Ile Leu Leu Leu Met Arg Arg Cys Val 115 Arg Ala Ser Gly Ser Gly Leu Leu Ser Thr Val Trp Lys Phe Ser Glu 135 Lys Leu Ser Val Ser Ser Val Leu Ala Thr Leu Val Ser Cys Leu Leu 145 150 155 Ser Val Leu Leu Arg Leu Arg Pro Pro Leu Leu Thr Ile Leu Thr 165 170 Leu Thr Leu Leu Arg Ala Gly 180 <210> 153 <211> 1011 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(988) <223> RXN00871 <400> 153 gggaaaaggc gatcaccagc cgttggctcg acccagcaac ccacggtggc attaacctcg 60 gtttcccaca gaacgattaa ttgaaggaga gcacaggact atg cgt tgg ttc cat 115 Met Arg Trp Phe His aag aag ggc gaa ctg gcc cga gat ggt tgg caa agc gtt gtc gat gcc 163 Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala ace ace cca ggt tgg gaa tat ace ggc ate ege att gee gaa etg gge 211 Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc 259 Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe 45 307 att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr 60 cat ctt cac gga aga aag tca gtc ttt gat gga cca acc gat gtg ctc 355 His Leu His Gly Arg Lys Ser Val Phe Asp Gly Pro Thr Asp Val Leu 75 80 tac ctc ccc act gga caa aca gca acg ctc agt ggt cag gga cga gtc 403 BGI-126CP - 232 -

Tyr	Leu	Pro	Thr	Gly 90	Gln	Thr	Ala	Thr	Leu 95	Ser	Gly	Gln	Gly	Arg 100	Val	
_	gtg Val		_	_			_	-		_			_			451
	cca Pro															499
_	caa Gln 135	-						_	_	_		_	_	_	_	547
	atc Ile															595
	cca Pro															643
	gaa Glu					-	_	_		_	_	_				691
_	gaa Glu	_	_	_		_			_							739
	gcg Ala 215											-		-		787
	cta Leu	_								_		_	_			835
	gac Asp	_					_	_	_			_	_		_	883
	tgg Trp															931
	acc Thr			-		-	-	_	_					-		979
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<212> PRT

<213> Corynebacterium glutamicum

<400> 154

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20 25 30

Ile Ala Glu Leu Gly Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly
35 40 45

Val Glu Arg Ile Phe Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His 50 55 60

His Gly Gln Val Thr His Leu His Gly Arg Lys Ser Val Phe Asp Gly 65 70 75 80

Pro Thr Asp Val Leu Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser 85 90 95

Gly Gln Gly Arg Val Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys 100 105 110

Glu Trp Lys Tyr Ile Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly
115 120 125

Ala Gly Arg Ser Ser Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala 130 135 140

Leu Asp Ala Ala Arg Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu 145 150 155 160

Asn Trp Ser Ser Tyr Pro Pro His Lys His Asp Glu His Ile Pro Gly
165 170 175

His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser 180 185 190

Arg Val Gly Gly Arg Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe 195 200 205

Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val 210 215 220

Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala 225 230 235 240

Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly
245 250 255

Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala 260 265 270

Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro 275 280 285

Tyr Glu Asn Ala Asn Lys Glu Gly 290 295

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Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser Arg Val Gly Gly Arg

185		190		195	
gcc gaa gca gca Ala Glu Ala Ala 200					
cca gcg ggg gag Pro Ala Gly Glu 215	lle Asp 1	_			
gcg cta gtt cct Ala Leu Val Pro 230					
tat gac ttg tad Tyr Asp Leu Tyr				Asp Pro G	
atc tgg ctg att Ile Trp Leu Ile 265	Asn Asp A		, ,,	, , ,	
tgg acc ggg caa Trp Thr Gly Glr 280	-		-		964
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	_		Leu Ala Arg 10		rp Gln 15
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<pre><213> Corynebac <400> 156 Met Arg Trp Phe 1 Ser Val Val Asg 20 Ile Ala Glu Leu 35 Val Glu Arg Ile 50 His Gly Gln Val 65 Pro Thr Asp Val Gly Gln Gly Arg 100 Glu Trp Lys Typ </pre>	His Lys I 5 Ala Thr I Gly Ser G Phe Ile F Thr His I 70 Leu Tyr I 85 Val Ala V Ile Ala F	Lys Gly Glu Thr Pro Gly 25 Gly Glu Ser 40 Pro Leu Gln 55 Leu His Gly Leu Pro Thr Val Ala Glu 105 Pro Ala Glu 120	Trp Glu Tyr Leu Glu Leu Gly Ser Phe 60 Arg Lys Ser 75 Gly Gln Thr 90 Ala Pro Thr Thr Pro Val	Thr Gly II 30 Asn Asp Th 45 Asp Val Ai Val Phe As Ala Thr Le S Gln Glu Pr 110 Glu Leu Ar 125	le Arg nr Gly la His sp Gly 80 eu Ser 95 ro Lys



	_		
145	150	155 160	
Asn Trp Ser Ser Tyr 165		Asp Glu His Ile Pro Gly 175	
His Glu Ser Lys Leu 180	Glu Glu Ile Tyr Tyr 185	Phe Glu Ser Ala Pro Ser 190	
Arg Val Gly Gly Arg 195	Ala Glu Ala Ala Glu 200	Gly Ala Phe Gly Met Phe 205	
Ser Thr Tyr Ser Ser 210	Pro Ala Gly Glu Ile 215	Asp Ile Asn Ala Met Val 220	
Tyr Ser Gly Asp Ile 225	Ala Leu Val Pro Phe 230	Gly Tyr His Gly Pro Ala 235 . 240	
Val Ala Ala Pro Gly 245		Leu Asn Val Met Ala Gly 255	
Pro Asp Pro Glu Arg 260	Ile Trp Leu Ile Asn 265	Asp Asp Pro Ala His Ala 270	
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	Glu Ile Ser Glu Leu	ggg tta ggt tgc atg agt Gly Leu Gly Cys Met Ser 20	163
		att att gaa agt gca att Ile Ile Glu Ser Ala Ile 35	211
		gat att tac gat caa gga Asp Ile Tyr Asp Gln Gly 50	259
gtt aat gaa gaa att		aaa aaa tat caa aat cot	307





355 gat gac atc gtt atc gga act aaa gtt gga aat cga tta act gac gat Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn Arg Leu Thr Asp Asp 70 75

gga cat atg acg tgg gat Gly His Met Thr Trp Asp 90

373

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<211> 91

<212> PRT

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<400> 158

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Leu Gly Cys Met Ser Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile

Ile Glu Ser Ala Ile Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp 40

Ile Tyr Asp Gln Gly Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys

Lys Tyr Gln Asn Arg Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn 70

Arg Leu Thr Asp Asp Gly His Met Thr Trp Asp

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<211> 376

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<223> FRXA02829

<400> 159

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cta aaa agt ggc atc gaa att tct gaa ctt ggg tta ggt tgc atg agt 163 Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly Leu Gly Cys Met Ser 10 20 15

tta ggc aca gat tat aaa aaa gcg caa cca att att gaa agt gca att 211 Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile Ile Glu Ser Ala Ile 25 30

	aat Asn															259
_	aat Asn 55	_	-		_			-							_	307
_	gac Asp		_					_			_			_	-	355
	cat His												•			376
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	0> 1		70		-	-		C 1	T 1	63	T 1		G.1	-	0.3	
Met 1	Gln	гуs	Asn	11e 5	Leu	ьys	ser	GIÀ	10	GIU	11e	ser	GIU	15	GIÀ	
Leu	Gly	Cys	Met 20	Ser	Leu	Gly	Thr	Asp 25	Tyr	Lys	Lys	Ala	Gln 30	Pro	Ile	
Ile	Glu	Ser 35	Ala	Ile	Asp	Asn	Gly 40	Ile	Thr	Tyr	Phe	Asp 45	Thr	Ala	Asp	
Ile	Tyr 50	Asp	Gln	Gly	Val	Asn 55	Glu	Glu	Ile	Val	Gly 60	Lys	Ala	Leu	Lys	
Lys 65	Tyr	Gln	Asn	Arg	Asp 70	Asp	Ile	Val	Ile	Gly 75	Thr	Lys	Val	Gly	Asn 80	
Arg	Leu	Thr	Asp	Asp 85	Gly	His	Met	Thr	Trp 90	Gly	Ser					
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	0> 10 caago		tgad	ccaco	cg tạ	gcago	gattt	gat	tgad	cttt	atta	acad	cca a	ataaq	ggctga	60
tta	gcgg	gaa a	aatti	cgc	cc aa	aaaca	aggga	a caa	atggt	gtt		aca Thr				115
	tat Tyr															163

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а

gac ggt gca ttt cac gta cca gat gag cag cag ttc act gac Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln Phe Thr Asp 265 270 275
tagtattctg taggtcatgg cat
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Lys Glu Gly Glu Ile Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu 20 25 30
Thr Asp Asn Asn Val Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe 35 40 45
Thr Pro Arg Asp Leu Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile 50 55 60
Pro Pro Glu Arg Ile Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu 65 70 75 80
Lys Ser Gln Val Lys Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly 85 90 95
Leu Thr Thr Ala Leu His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn 100 105 110
Pro Glu Phe Val Val Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala 115 120 125
Ile Thr Thr Ala Ile Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys 130 135 140
Thr Asn Pro Asp Val Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala 145 150 155 160
Thr Gly Ser Val Ala Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro 165 170 175
Tyr Tyr Ile Gly Lys Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn 180 185 190
Thr Ile Gly Ala His Ser Glu His Thr Val Met Ile Gly Asp Arg Met 195 200 205
Asp Thr Asp Val Lys Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu 210 215 220
Val Arg Ser Gly Ile Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe 225 230 235 240
Arg Pro Thr His Val Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp 245 250 255

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Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile Lys Glu Gly Glu Ile
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Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe Thr Pro Arg Asp Leu
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Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile Pro Pro Glu Arg Ile
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Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu Lys Ser Gln Val Lys
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Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly Leu Thr Thr Ala Leu
cat acc gcg ggt tgg att ttg acg gat gca aat cct gag ttt gtt
                                                                   451
His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn Pro Glu Phe Val Val
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Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala Ile Thr Thr Ala Ile
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                            125
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								agc Ser 270								931
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Asn Ser Val Asp Ile Met Met Gly Thr Gly Gly Thr Pro Glu Gly Ile 210 215 220 Ile Thr Ala Cys Ala Met Lys Cys Met Gly Glu Ile Gln Gly Ile 230 235 Leu Ala Pro Met Asn Asp Phe Glu Arg Gln Lys Ala His Asp Ala Gly Leu Val Leu Asp Gln Val Leu His Thr Asn Asp Leu Val Ser Ser Asp 265 Asn Cys Tyr Phe Val Ala Thr Gly Val Thr Asn Gly Asp Met Leu Arg 275 280 285 Gly Val Ser Tyr Arg Ala Asn Gly Ala Thr Thr Arg Ser Leu Val Met Arg Ala Lys Ser Gly Thr Ile Arg His Ile Glu Ser Val His Gln Leu 305 315 310 Ser Lys Leu Gln Glu Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr 325 330 <210> 167 <211> 1035 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1012) <223> RXN02920 <400> 167 tgcatgcaga ttatctgtcc aactacgcca gccgcqcgta aagcgcgggc ctgctggtgg 60 cgggtggcgt cgaaaagcat ttttaaagga gtttaagacg atg aag ttt gtt atg 115 Met Lys Phe Val Met tat ecg cat ttg tgg gag tee acg acc get gte att gag ggt gge gga 163 Tyr Pro His Leu Trp Glu Ser Thr Thr Ala Val Ile Glu Gly Gly Gly 10 15 cat gag cgg gtt gag gat att aaa gat gca gac ttc att ttc ttt aat 211 His Glu Arg Val Glu Asp Ile Lys Asp Ala Asp Phe Ile Phe Phe Asn 25 ggt tca gcg ccg gag ttc ccg gat ttg ccg gag aac atc aag ttc gtg 259 Gly Ser Ala Pro Glu Phe Pro Asp Leu Pro Glu Asn Ile Lys Phe Val 40 45 cag gcc tcc atg gcg ggt att gat gcg ctg gtc aag cgt ggt gtc gtc 307 Gln Ala Ser Met Ala Gly Ile Asp Ala Leu Val Lys Arg Gly Val Val 55 60 65 aat gag aag gca cgt tgg gca aac gcg gct ggc ctg tac gct gac acc 355 Asn Glu Lys Ala Arq Trp Ala Asn Ala Ala Gly Leu Tyr Ala Asp Thr

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	_				-	aat Asn				_	_		-		-	595
_	_			_	_	gat Asp	_	_	-				_		_	643
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_		_	_		_	ggc Gly	-	-	-			-			-	739
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Phe Ile Phe Phe Asn Gly Ser Ala Pro Glu Phe Pro Asp Leu Pro Glu 35 40 45

Asn Ile Lys Phe Val Gln Ala Ser Met Ala Gly Ile Asp Ala Leu Val 50 55 60

Lys Arg Gly Val Val Asn Glu Lys Ala Arg Trp Ala Asn Ala Ala Gly 65 70 75 80

Leu Tyr Ala Asp Thr Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala 85 90 95

Gln Met His Met His Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val 100 105 110

Arg Pro Glu Val Glu Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr 115 120 125

Val Ala Ile Leu Gly Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met 130 135 140

Leu Lys Pro Phe Asn Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg 145 150 155 160

Pro Val Glu Gly Ala Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His 165 170 175

Val Trp Ala Glu Ala Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp 180 185 190

Ala Thr Tyr Gln Ile Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro 195 200 205

Ser Ala Val Val Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp 210 215 220

Asp Leu Val Asp Ala Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu 225 230 235 240

Asp Val Thr Asp Pro Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu 245 250 255

Met Asp Asn Val Val Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg 260 265 270

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290 295 300

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														aat Asn 145		489
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Ala Gly Gly I 65	Ile Gly Val 70	Arg Leu Leu	Glu Met Leu Ly: 75	s Pro Phe Asn 80	
Val Lys Thr I	Ile Ala Val 85	Asn Asn Ser	Gly Arg Pro Va.	l Glu Gly Ala 95	
-	Phe Ala Met 100	Asp Lys Ala 105	Glu His Val Tr	Ala Glu Ala 110	
Asp Val Phe V	Val Leu Ile	Leu Pro Leu 120	Thr Asp Ala Th	-	
Val Asn Ala G 130	Glu Thr Leu	Gly Lys Met 135	Lys Pro Ser Ala	a Val Val Val	
Asn Val Gly A	Arg Gly Pro 150	Leu Ile Asn	Thr Asp Asp Let	ı Val Asp Ala 160	
Leu Asn Asn G	Gly Thr Ile 165	Ala Gly Ala	Ala Leu Asp Val	l Thr Asp Pro 175	

Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val
180 185 190

Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr
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att ttg cta cga cac ggg cag act cac aac aac gtc aaa cac ctc ctg $\,$ 163 Ile Leu Leu Arg His Gly Gln Thr His Asn Asn Val Lys His Leu Leu $\,$ 10 $\,$ 15 $\,$ 20

gac acc cgc cca cca gga gct gaa ctc acc gac ctg ggc cgt aaa caa 211 Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp Leu Gly Arg Lys Gln 25 30 35

gcc ctt gaa gtt ggc cac gaa cta gcc acc tac tcc ggt gag cgc ctc 259
Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr Ser Gly Glu Arg Leu
40 45 50

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ttt gaa atg cgc ggc gat gaa gaa gcc cac atg aat tac tcc cgc gca 451 Phe Glu Met Arg Gly Asp Glu Glu Ala His Met Asn Tyr Ser Arg Ala 105 110 115

ctc aac ggc tgg ctt cac ggg gat cct gcc gct ggt ctt ccc ggc ggt 499 Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala Gly Leu Pro Gly Gly

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His	Ala	Thr	Gly 180	Val	Asp	Pro	Asn	Phe 185	Ala	Phe	Asn	Thr	Туг 190	Leu	Gly	
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	ttt Phe												Asp			163
	acc Thr		_		_		-	-	-						_	211
	atc Ile															259
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Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe 20 25 30

Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu 35 40 45

Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile 50 55 60

Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp 65 70 75 80

Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu 85 90

<210> 179

<211> 1953

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<223> RXN02591

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Met Thr Ala Ala

1

atc agg ggc ctt cag ggc gag gcg ccg acc aag aat aag gaa ctg ctg 163
Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys Asn Lys Glu Leu Leu
10 15 20

aac tgg atc gca gac gcc gtc gag ctc ttc cag cct gag gct gtt gtg 211 Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln Pro Glu Ala Val Val

ttc gtt gat gga tcc cag gct gag tgg gat cgc atg gcg gag gat ctt 259
Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg Met Ala Glu Asp Leu
40 45 50

gtt gaa gcc ggt acc ctc atc aag ctc aac gag gaa aag cgt ccg aac 307 Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu Glu Lys Arg Pro Asn

agc tac cta gct cgt tcc aac cca tct gac gtt gcg cgc gtt gag tcc 355 Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val Ala Arg Val Glu Ser

cgc acc ttc atc tgc tcc gag aag gaa gaa gat gct ggc cca acc aac 403 Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp Ala Gly Pro Thr Asn 90 95 100

aac tgg gct cca cca cag gca atg aag gac gaa atg tcc aag cat tac 451 Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu Met Ser Lys His Tyr 105 110 115

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ggt Gly	cca Pro 135	atc Ile	agc Ser	gat Asp	ccg Pro	gac Asp 140	cct Pro	aag Lys	ctt Leu	ggt Gly	gtg Val 145	cag Gln	ctc Leu	act Thr	gac Asp	547
													atg Met			595
_		_	_	_						_		-	agg Arg	_		643
		_		_		_				_	_	_	gtt Val 195	_		691
	_		_		_				_				acc Thr	_	_	739
											_		ctg Leu	_	_	787
													gaa Glu			835
	_				_			_		_			cca Pro			883
_					-	-	_				_	_	ggc Gly 275	_		931
													gct Ala			979
													ggc Gly			1027
													ggc Gly			1075
	-						_	_		-	-		ggc Gly			1123
_					-			-	_		_		tgg Trp 355		_	1171

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-						gac Asp 380	_		_	_					_	1267
						cag Gln										1315
						atc Ile								_	_	1363
_	_		_		_	gtt Val		_			_					1411
						ctc Leu										1459
						ctc Leu 460										1507
					-	ggt Gly	_		_	_				_	_	1555
		-			_	aag Lys	_					_	_			1603
	_	_		_	_	gga Gly	_		_						-	1651
						tgg Trp										1699
						gtt Val 540										1747
_		_			_	acc Thr				- ,	_	_	_	_	_	1795
						tgg Trp										1843
						cca Pro	_	_		_		_		-	_	1891
ttc	gat	gct	ctg	aag	gcc	cgc	att	tca	gca	gct	cac	gct	taaa	gtto	ac	1940

Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala His Ala 600 605 610

gcttaagaac tgc

1953

<210> 180

<211> 610

<212> PRT

<213> Corynebacterium glutamicum

<400> 180

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Asn Lys Glu Leu Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln
20 25 30

Pro Glu Ala Val Val Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg 35 40 45

Met Ala Glu Asp Leu Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu 50 55 60

Glu Lys Arg Pro Asn Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val 65 70 75 80

Ala Arg Val Glu Ser Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp
85 90 95

Ala Gly Pro Thr Asn Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu 100 105 110

Met Ser Lys His Tyr Ala Gly Ser Met Lys Gly Arg Thr Met Tyr Val 115 120 125

Val Pro Phe Cys Met Gly Pro Ile Ser Asp Pro Asp Pro Lys Leu Gly 130 135 140

Val Gln Leu Thr Asp Ser Glu Tyr Val Val Met Ser Met Arg Ile Met 145 150 155 160

Thr Arg Met Gly Ile Glu Ala Leu Asp Lys Ile Gly Ala Asn Gly Ser 165 170 175

Phe Val Arg Cys Leu His Ser Val Gly Ala Pro Leu Glu Pro Gly Gln 180 185 190

Glu Asp Val Ala Trp Pro Cys Asn Asp Thr Lys Tyr Ile Thr Gln Phe 195 200 205

Pro Glu Thr Lys Glu Ile Trp Ser Tyr Gly Ser Gly Tyr Gly Gly Asn 210 215 220

Ala Ile Leu Ala Lys Lys Cys Tyr Ala Leu Arg Ile Ala Ser Val Met 225 230 235 240

Ala Arg Glu Glu Gly Trp Met Ala Glu His Met Leu Ile Leu Lys Leu 245 250 255

Ile Asn Pro Glu Gly Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser

260 265 270 Ala Cys Gly Lys Thr Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly 280 Trp Thr Ala Gln Val Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg 295 Glu Asp Gly Leu Tyr Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val 310 315 Ala Pro Gly Thr Asn Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met 325 Glu Pro Gly Asn Thr Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly Asp Ile Trp Trp Glu Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile Asp Trp Met Gly Asn Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala 375 His Pro Asn Ser Arg Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala 395 Ala Pro Glu Phe Asn Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu Phe Gly Gly Arg Arg Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr Asp Trp Glu His Gly Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln Thr Ala Ala Ser Ala Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro 455 Met Ala Met Leu Pro Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln Asn Trp Ile Asp Met Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile Phe Leu Val Asn Trp Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp Pro Gly Phe Gly Asp Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg Ile Glu Gly His Val Gly Ala Asp Glu Thr Val Val Gly His Thr Ala Lys Ala Glu Asp Leu Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp 550 555 Val Lys Glu Ala Leu Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val 565 Glu Asp Asn Ala Glu Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala 580 585 590

120

135

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125

140

cca aat gaa gat gct gaa gtc tcc aag gtt att gca aag gcc tac aag

Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys

130

547

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_			_		_		_	_		_	aag Lys	_			_	643
_						_	_	_	-	_	gtt Val		-			691
-		_	-						_		act Thr		_	_		739
		_		_				-	_		atg Met 225	-			_	787
											aag Lys					835
	_	-	-	-	_			-	_	_	gag Glu			_		883
_	_		_				_		_	_	atg Met		_	_		931
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	-				_	_		_	_	_	act Thr	_			_	1075
											ctc Leu					1123
											ttg Leu					1171
											agc Ser					1219
											cac His 385					1267
cac	atg	atc	aac	ttc	taga	aatco	cac o	ctcgt	tggd	cc ct	-g					1305

His Met Ile Asn Phe 390

<210> 182

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 182

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Ile Glu Ile His Gly Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu 35 40 45

Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys 50 55 60

Ile Ile Ala Thr Gly Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe 65 70 75 80

Ser Glu Asn Val Val Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala 85 90 95

Pro Lys Lys Met Val Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe
100 105 110

Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe 115 120 125

Met Asp Arg Val Leu Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile 130 135 140

Ala Lys Ala Tyr Lys Lys Met Gly Val Lys Leu Leu Pro Gly His Ala 145 150 155 160

Thr Thr Ala Val Arg Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln
165 170 175

Lys Lys Gly Ser Asp Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met 180 185 190

Val Ser Val Gly Phe Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn 195 200 205

Thr Gly Val Lys Leu Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr 210 215 220

Met Arg Thr Asn Val Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala 225 230 235 240

Lys Leu Gln Leu Ala His Val Ala Glu Ala Gln Gly Ile Val Ala Ala 245 250 255

Glu Thr Ile Ala Gly Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met 260 265 270

- 264 -BGI-126CP Met Pro Arg Ala Thr Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr Thr Glu Glu Gln Ala Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val 295 Ala Ser Phe Pro Phe Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu 315 Thr Asp Gly Phe Ala Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu 325 330 Leu Gly Ala His Leu Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu 345 Leu Val Leu Ala Gln Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg 355 360 Ser Val His Ile His Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly His Met Ile Asn Phe 390 <210> 183 <211> 294 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(271) <223> RXS01261 <400> 183 gtgggtgttt ttcattttct tccactctaa aattaagtat ggaaaaccaa ccgcacccgg 60 atgcacgaca atgacccact aaacacgtat ccttgaatgc gtg act gaa cat tat 115 Val Thr Glu His Tyr gac gta gta gta ctc gga gcc ggc ccc ggt ggc tat gtc tcc gcc atc 163 Asp Val Val Leu Gly Ala Gly Pro Gly Gly Tyr Val Ser Ala Ile cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac 211 Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct 259 Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser

gat caa aaa cgc tgaagttgcc cataccttta ccc Asp Gln Lys Arg 55 294

<210> 184 <211> 57 <212> PRT <213> Corynebacterium glutamicum

<400> 184

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Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val 20 25 30

Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile $35 \hspace{1cm} 40 \hspace{1cm} 45$

Pro Ser Lys Val Ser Asp Gln Lys Arg 50 55

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<211> 1650

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<223> RXA02640

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 Met Arg Ile Ser Lys

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- gcc aat gcg tat gtt gca gcg att gac caa ggc acc act tcc act cgg 163 Ala Asn Ala Tyr Val Ala Ala Ile Asp Gln Gly Thr Thr Ser Thr Arg
- tgc atc ttc att gat gcc caa gga aaa gtg gtg tct tct gct tcc aag 211 Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val Ser Ser Ala Ser Lys
- gag cac cgc caa atc ttc cca caa cag ggc tgg gta gag cac gat cct 259 Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp Val Glu His Asp Pro
- gaa gaa att tgg gac aac att cga tct gtc gtc agc cag gcg atg gtc 307 Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val Ser Gln Ala Met Val
- tcc att gac atc acc cca cac gag gtt gca tcg ctg gga gtc acc aac 355 Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser Leu Gly Val Thr Asn 70 75 80 85
- cag cgc gaa acc acc gtg gtg tgg gac aag cac acc ggc gaa cct gtc 403 Gln Arg Glu Thr Thr Val Val Trp Asp Lys His Thr Gly Glu Pro Val
- tac aac gca atc gtg tgg caa gac acc cgc acc tct gac att tgc cta 451
 Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr Ser Asp Ile Cys Leu
 105 110 115

and the filler has been a fact to

							cag Gln 125						499
							tcg Ser						547
							gaa Glu						595
							gtg Val						643
_		-	•		-	-	gcc Ala		_	-	_		691
-		-			_	-	gat Asp 205	-	_	_		-	739
_			-	-		-	att Ile						787
_			_		-		cgc Arg		-				835
-	-	-	_				gtg Val						883
		_					gaa Glu	 _	_				 931
							aac Asn 285						979
							atc Ile						1027
							tcc Ser						1075
							cag Gln						1123
							gaa Glu						1171

	_				ctg Leu		_		_		-		-	_	_	1219
	_				ctc Leu		_		_		_				_	1267
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					gca Ala											1363
					aat Asn											1411
					caa Gln											1459
	-	_		_	gca Ala											1507
_			_		ctt Leu 475		_		_		_				_	1555
					cgc Arg											1603
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<211> 509

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

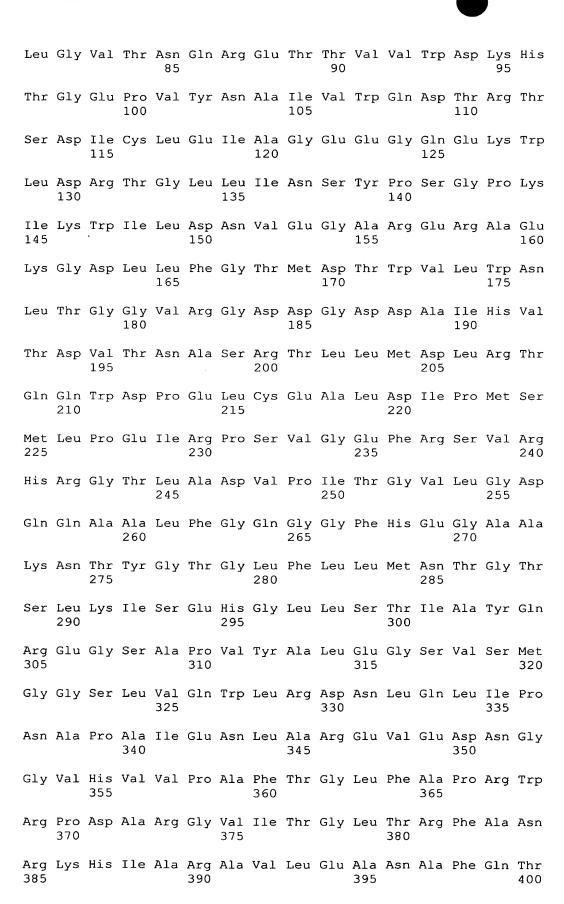
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Thr Thr Ser Thr Arg Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val

Ser Ser Ala Ser Lys Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp 40

Val Glu His Asp Pro Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val 50 55

Ser Gln Ala Met Val Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser 70 75





Arg Glu Val Val Asp Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu 405 410 415

Ser Leu Arg Val Asp Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln

Met Gln Ala Asp Phe Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val
435
440
445

Glu Thr Thr Ala Val Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly 450 455 460

Phe Phe Lys Thr Thr Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys 465 470 475 480

Val Trp Asn Pro Asp Met Ser Glu Glu Glu Arg Glu Arg Tyr Ala 485 490 495

Glu Trp Asn Arg Ala Val Glu His Ser Tyr Asp Gln Ala 500 505

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<223> RXN01025

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ctgagacggt taaatatcgt tttcgaaagg tgggtttcgc gtg gtt tct gta agc 115 Val Val Ser Val Ser 1 5

gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct $\,$ 163 Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser $\,$ 10 $\,$ 15 $\,$ 20

gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca 211 Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala 25 30 35

agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att 259 Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile 40 45 50

acg ttg ccg gag tcg ctg cag gtc aca tca tcg gca acg gag gct tta 307
Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu
55 60 65

gag ggc gca gcc att gtg gtg ttg gcg att cct tcg cag gcg ttg cgt 355 Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg 70 75 80 85

ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg 403 Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu

				90)				95	.				100)	
gtg Val	tcc Ser	ttg Leu	gct Ala 105	Lys	ı ggt Gly	att Ile	gaa Glu	aag Lys 110	ggc	acg Thr	cac	ctg Leu	cgg Arg 115	Met	agt Ser	451
gaa Glu	gtg Val	ato Ile 120	Ala	gag Glu	gtg Val	acg Thr	gaa Glu 125	gcg Ala	gat Asp	cct Pro	tca Ser	cgc Arg 130	Ile	gcg Ala	gtg Val	499
ttg Leu	tcg Ser 135	Gly	cca Pro	aac Asn	ctt Leu	gct Ala 140	cgt Arg	gag Glu	atc	gcg Ala	gag Glu 145	Gly	cag Gln	cct Pro	gca Ala	547
gct Ala 150	Thr	gtg Val	att Ile	gct Ala	tgc Cys 155	cct Pro	gat Asp	gaa Glu	aac Asn	cga Arg 160	gcg Ala	aaa Lys	ctt Leu	gtg Val	cag Gln 165	595
gct Ala	gca Ala	gtg Val	gct Ala	gcg Ala 170	ccg Pro	tat Tyr	ttc Phe	cgc Arg	ccg Pro 175	tac Tyr	acc Thr	aac Asn	act Thr	gat Asp 180	gtg Val	643
gtg Val	ggc Gly	act Thr	gaa Glu 185	atc Ile	ggt Gly	ggt Gly	gcg Ala	tgt Cys 190	aag Lys	aac Asn	gtc Val	atc Ile	gcg Ala 195	ctg Leu	gcc Ala	691
tgt Cys	ggt Gly	att Ile 200	tcc Ser	cat His	ggt Gly	tac Tyr	ggc Gly 205	ctg Leu	ggt Gly	gag Glu	aac Asn	acc Thr 210	aat Asn	gca Ala	tcg Ser	739
ttg Leu	att Ile 215	act Thr	cgt Arg	ggc Gly	ctt Leu	gca Ala 220	gag Glu	atc Ile	gca Ala	cgc Arg	ctc Leu 225	ggt Gly	gcc Ala	aca Thr	ttg Leu	787
ggt Gly 230	gcg Ala	gat Asp	gcg Ala	aag Lys	act Thr 235	ttt Phe	tct Ser	ggc Gly	ctt Leu	gcg Ala 240	gga Gly	atg Met	ggc Gly	gac Asp	ttg Leu 245	835
gtg Val	gct Ala	acg Thr	tgt Cys	tca Ser 250	tca Ser	ccg Pro	ctg Leu	tcg Ser	cgt Arg 255	aac Asn	cgc Arg	agc Ser	ttc Phe	ggt Gly 260	gag Glu	883
cgt Arg	ttg Leu	ggt Gly	cag Gln 265	ggt Gly	gaa Glu	tcc Ser	cta Leu	gag Glu 270	aag Lys	gct Ala	cgc Arg	gag Glu	gca Ala 275	acc Thr	aat Asn	931
ggt Gly	cag Gln	gtt Val 280	gcg Ala	gag Glu	ggt Gly	gtt Val	att Ile 285	tcc Ser	tcg Ser	cag Gln	tcg Ser	att Ile 290	ttt Phe	gat Asp	ctt Leu	979
gcc Ala	acc Thr 295	aag Lys	ctt Leu	ggt Gly	gtg Val	gag Glu 300	atg Met	ccg Pro	atc Ile	acc Thr	cag Gln 305	gct Ala	gtc Val	tac Tyr	ggt Gly	1027
gtg Val 310	tgc Cys	cac His	cga Arg	gat Asp	atg Met 315	aaa Lys	gta Val	act Thr	gac Asp	atg Met 320	att Ile	gtg Val	gct Ala	Leu	atg Met 325	1075
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<211>.332

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

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Ala Lys Val Phe Ser Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg 20 25 30

Arg Glu Glu Leu Ala Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp 35 40 45

Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser 50 55 60

Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro 65 70 75 80

Ser Gln Ala Leu Arg Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro 85 90 95

Gln Asp Ala Thr Leu Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr 100 105 110

His Leu Arg Met Ser Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro 115 120 125

Ser Arg Ile Ala Val Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala 130 135 140

Glu Gly Gln Pro Ala Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg 145 150 155 160

Ala Lys Leu Val Gln Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr 165 170 175

Thr Asn Thr Asp Val Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn 180 185 190

Val Ile Ala Leu Ala Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu 195 200 205

Asn Thr Asn Ala Ser Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg 210 215 220

Leu Gly Ala Thr Leu Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala 225 230 235 240

Gly Met Gly Asp Leu Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn 245 250 255

Arg Ser Phe Gly Glu Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala 260 265 270

Arg Glu Ala Thr Asn Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln 275 280 285



Ser Ile Phe Asp Leu Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr 290 295 300

Gln Ala Val Tyr Gly Val Cys His Arg Asp Met Lys Val Thr Asp Met 305 310 315 320

Ile Val Ala Leu Met Gly Arg Ser Lys Lys Ala Glu 325 330

<210> 189

<211> 1015

<212> DNA

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<221> CDS

<222> (101)..(1015)

<223> FRXA01025

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gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct 163 Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser 10 15 20

gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca 211 Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala 25 30 35

agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att 259 Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile 40 45 50

acg ttg ccg gag tcg ctg cag gtc aca tca tcg gca acg gag gct tta 307
Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu
55 60 65

gag ggc gca gcc att gtg gtg ttg gcg att cct tcg cag gcg ttg cgt 355 Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg 70 75 80 85

ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg 403 Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu 90 95 100

gtg tcc ttg gct aaa ggt att gaa aag ggc acg cac ctg cgg atg agt 451 Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr His Leu Arg Met Ser 105 110 115

gaa gtg atc gcg gag gtg acg gaa gcg gat cct tca cgc atc gcg gtg 499 Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro Ser Arg Ile Ala Val 120 125 130

ttg tcg ggg cca aac ctt gct cgt gag atc gcg gag ggg cag cct gca 547

Leu Ser Gly	Pro Asn Leu	Ala Arg Glu	Ile Ala Glu	Gly Gln Pro	Ala
135		140	145		505
	-		aac cga gcg Asn Arg Ala 160		-
		_	ccg tac acc Pro Tyr Thr 175	_	Val
			aag aac gtc Lys Asn Val		
			ggt gag aac Gly Glu Asn		
_			gca cgc ctc Ala Arg Leu 225		-
			ctt gcg gga Leu Ala Gly 240		
			cgt aac cgc Arg Asn Arg 255		Glu
			aag gct cgc Lys Ala Arg		
		-	tcg cag tcg Ser Gln Ser	_	
			atc acc cag Ile Thr Gln 305		1015
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Arg Glu Glu 35	Leu Ala Ser	Thr Ile Arg	Asp Ser His	Glu Asn Arg	Asp
Tyr Leu Pro 50	Gly Ile Thr	Leu Pro Glu 55	Ser Leu Gln 60	Val Thr Ser	Ser

Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro 65 70 75 80

Ser Gln Ala Leu Arg Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro 85 90 95

Gln Asp Ala Thr Leu Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr 100 105 110

His Leu Arg Met Ser Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro 115 120 125

Ser Arg Ile Ala Val Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala 130 135 140

Glu Gly Gln Pro Ala Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg 145 150 155 160

Ala Lys Leu Val Gln Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr 165 170 175

Thr Asn Thr Asp Val Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn 180 185 190

Val Ile Ala Leu Ala Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu 195 200 205

Asn Thr Asn Ala Ser Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg 210 215 220

Leu Gly Ala Thr Leu Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala 225 230 235 240

Gly Met Gly Asp Leu Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn 245 250 255

Arg Ser Phe Gly Glu Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala 260 265 270

Arg Glu Ala Thr Asn Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln 275 280 285

Ser Ile Phe Asp Leu Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr 290 295 300

Gln 305

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<211> 1809

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<220>

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<223> RXA01851

<400> 191

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ttt gaa tcc co Phe Glu Ser An			-		•	_	Val	163
att gtg att gg Ile Val Ile Gl								211
caa ggc cgc gg Gln Gly Arg Gl 40	_		-		-	-		259
tct gga aca to Ser Gly Thr Se 55								307
tat ttg gag ca Tyr Leu Glu Gl 70								355
cgc cgg tac ct Arg Arg Tyr Le							Ser	403
ttc atg ctc ac Phe Met Leu Th 10	r Ala Phe			_	-	_	_	451
ggt gct ggt gt Gly Ala Gly Va 120		_				_	_	499
ggg caa tcg aa Gly Gln Ser Ly 135				Phe A				547
aat gca ctg ct Asn Ala Leu Le 150		-		_				595
gga gcg tgg cg Gly Ala Trp An							Leu	643
ctc ctc gcg gt Leu Leu Ala Va 18	l lle Lys							691
aac cac gcc aa Asn His Ala Ly 200								739
gtc aag ggt gt Val Lys Gly Va 215				Thr A				787

		_				atc Ile		_			_		-		_	835
	_		_	_		gag Glu	_		_	_	_		_			883
_				_		act Thr		-	_		_	_	_			931
						ggc Gly										979
						cca Pro 300										1027
_	-		_	_	_	gaa Glu	_	_		_	_	_				1075
	-	_	_	_	_	aca Thr	_		_	_						1123
						ccg Pro										1171
_			_			gat Asp			_		_		-			1219
-		_			_	tct Ser 380			_					_		1267
						gag Glu										1315
		_	_	_		ttt Phe	_			_	_	_	_	_		1363
						tcc Ser										1411
						gat Asp										1459
_	_	_				gag Glu 460		_			_	_		_	-	1507

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					ggg Gly 475											1555
					ttt Phe											1603
	-		_	_	cgt Arg	_					_	_				1651
					cgt Arg											1699
			_		ctt Leu		_	_	_	_	_				_	1747
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tcat	cgad	cac o	cgg													1809
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Asp	Asn	Tyr	Asp 20	Val	Ile	Val	Ile	Gly 25	Gly	Gly	Ile	Ser	Gly 30	Val	Gln	
Ile	Ala	Arg 35	His	Ala	Gln	Gly	Arg 40	Gly	Leu	Arg	Thr	Val 45	Met	Phe	Glu	
Ala	Arg 50	Asp	Tyr	Ser	Ser	Gly 55	Thr	Ser	Ser	Thr	Thr 60	Ser	Lys	Met	Ile	
His 65	Gly	Gly	Leu	Arg	Tyr 70	Leu	Glu	Gln	Tyr	Asp 75	Phe	Gly	Val	Val	Gln 80	
Glu	Ala	Val	Lys	Glu 85	Arg	Arg	Tyr	Leu	Gly 90	Ile	Ala	Ala	Pro	His 95	Leu	
Val	Ala	Pro	Arg 100	Ser	Phe	Met	Leu	Thr 105	Ala	Phe	Asp	Trp	Ser 110	Glu	Pro	
Lys	Ala	Pro 115	Met	Leu	Gly	Ala	Gly 120	Val	Ala	Leu	Tyr	Glu 125	Thr	Met	Ala	
							_	_		_	•	_	_	_		
Trp	Gln 130	Arg	Asn	Gln	Gly	Gln 135	Ser	Lys	Glu	Asn	His 140	Ser	Pro	Arg	Phe	

145 150 155 160 Pro Glu Gly Leu Lys Gly Ala Trp Arg His Asp Asp Thr Leu Asn Leu 170 His Ala Glu Arg Leu Leu Ala Val Ile Lys Ala Phe Ala Ala Asp 180 185 Gly Gly Thr Ala Ile Asn His Ala Lys Val Thr Arg Ile Leu Arg Asn 200 Val Glu Glu Gly Arg Val Lys Gly Val Glu Val Thr Asp Gln Val Thr Asn Thr Thr His Glu Val Asn Ala Pro Val Val Ile Asn Ala Ala Gly Pro Trp Val Ala Gln Ala Leu Gly Asp Leu Ala Glu Val Thr Lys Leu Lys Val Arg Gln Ser Lys Gly Val His Leu Leu Thr Gly Asp Leu Gly Ser Gln Ser Gly Val Phe Val Arg Gly Lys Asn Gly Lys His Val Ile Val Asn Pro Trp Met Gly Arg Thr Leu Ile Gly Pro Thr Asp Thr Met 295 Ile Asp Gly Asp Ala Asp Asp Ala Ala Asp Glu Ser Asp Ile Asp 310 315 Leu Leu Clu Thr Ile Asp Ser Val Arg Ala Thr Pro Leu Asp Arg 325 330 Lys Glu Ile Ile Ser Thr Leu Val Gly Val Arg Pro Leu Val Asp Asp 345 Gly Thr Asp Thr Tyr Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His Ala Asn Val Gly Ile Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp 375 Thr Thr Ser Arg Val Met Gly Tyr Lys Val Ile Glu His Val Val Glu His Gln Ala Ala Val Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln Met Pro Leu Ser Thr Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser 420 425 Phe Glu Ser Ala Leu Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu 440 Ile Arg Val His Leu Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val 450 455 Leu Asp Leu Val Ala Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro 470 475

70

Asp Asn Leu Asp Ile Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu 485 Ala Ala Val Asp Leu Ala Asp Val Leu Asp Arg Arg Ile Val Leu Gly Thr Leu Gly Tyr Val Gln Pro Ala Ala Val Arg Ala Thr Ala Glu Ala Met Ala Gln Val Thr Gly Trp Ser Ala Glu Leu Ile Asp Ala Gln Cys 535 Gln Ser Tyr Leu Ala Lys Gln Asp Lys Ile Gln Ala Val Leu Lys Pro 555 Tyr Arg <210> 193 <211> 900 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(877) <223> RXA01242 <400> 193 cgccggcaac caaatgaggc ttttgggcgt tggacagtga gacaatgggt aagaaattcg 60 gacatattta gtaaattggc tttttgcttt aaggagtgac atg tac gca gag gag 115 Met Tyr Ala Glu Glu cgc cgt cga cag att gcc tca tta acg gca gtt gag gga cgt gta aat 163 Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val Glu Gly Arg Val Asn gtc aca gaa tta gcg ggc cga ttc gat gtc act gca gag acg att cga 211 Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr Ala Glu Thr Ile Arg 25 259 cga gac ctt gcg gtg cta gac cgc gag gga att gtt cac cgc gtt cac Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile Val His Arg Val His ggt ggc gca gta gcc acc caa tct ttc caa acc aca gag ttg agc ttg 307 Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr Thr Glu Leu Ser Leu 55 60

gat act cgt ttc agg tct gca tcg tca gca aag tac tcc att gcc aag

Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys Tyr Ser Ile Ala Lys

gca gcg atg cag ttc ctg ccc gct gag cat ggc gga ctg ttc ctc gat

Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly Gly Leu Phe Leu Asp

90

355

403

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	gga Gly															451
-	tcc Ser	_	_		_					_				_		499
	ctg Leu 135	_		_			_	-	_	_	_				_	547
-	cgc Arg				-	_	_			_				_		595
	gcg Ala	_	_	_		_	_								_	643
_	ttg Leu	_			_		-		_				_	_	_	691
	tct Ser		_				_		_				_	_	-	739
	acc Thr 215	_	-			-				_			-		-	787
_	atc Ile	_	_	-	_		_			-		_	_		_	835
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Glu	Glv	Δκα	Val	Asn	Val	Thr	Glu	Lau	Δla	Glv	Δνα	Phe	Asn	Val	ሞb r	

Val His Arg Val His Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr 50 55 60

Thr Glu Leu Ser Leu Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys Tyr Ser Ile Ala Lys Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly 85 90 Gly Leu Phe Leu Asp Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu 105 Ile Ser Glu His Pro Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys 115 Leu Pro Ile Ala Leu Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln 135 Leu Leu Gly Gly Ser Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp 145 150 Thr Ala Leu Arg Thr Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile 165 170 Gly Thr Asn Ala Leu Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser Gln Glu Ala Ala Met Lys Ser Ala Met Ile Thr Asn Ala His Lys Val 200 Val Val Leu Cys Asp Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser 215 Phe Gly Ala Ile Ser Asp Ile Asp Val Val Thr Asp Ala Gly Ala 230 235 Pro Ala Ser Phe Val Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val 250 Ile Ala Glu <210> 195 <211> 969 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(946) <223> RXA02288 <400> 195 aacaacaatc taacgccatc atgttataaa aaagcaagac ctaacataaa aatgttagaa 60 agtgctggat ctaacaacat ttccgtggta actttttcac atg tcc caa gtg att 115 Met Ser Gln Val Ile

Met Ser Gln Val Ile

1 5

ccc gcc agc tca caa gaa aag cgt cgt gag cgc atc gtt tct tat gtc 163

Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg Ile Val Ser Tyr Val

10 15 20

										tta Leu						211
-										gag Glu						259
										cgt Arg						307
										cat His 80						355
			_	_		-	-			ttg Leu		-			_	403
										gag Glu						451
										acg Thr						499
										agc Ser						547
										gat Asp 160						595
										gcg Ala						643
										gtt Val						691
	_	_		-	_	_	_	_		gcg Ala	_					739
										aaa Lys						787
		_	_	_	_					gac Asp 240					_	835
_	-	_		_		_		-		ttg Leu	_		_	_		883
cag	atc	cat	gtg	att	gac	cac	aat	ggt	gat	gaa	att	ttg	gat	acc	cca	931

Gln Ile His Val Ile Asp His Asn Gly Asp Glu Ile Leu Asp Thr Pro 265 270 275

acg gaa gag gat ttt taagatggct ttggttcttg gaa Thr Glu Glu Asp Phe 280 969

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<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 196

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Ala Glu Leu Phe Glu Val Ser Ala Met Thr Ile His Arg Asp Leu Glu 35 40 45

Ala Leu Ala Ala Asp Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg 50 55 60 .

Ser Val Ser Pro Ser Met Ser Glu Leu Ala Val Glu Gln Arg Arg His 65 70 75 80

Leu His Arg Thr Val Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu 85 90 95

Ile Pro Glu Gly Ala Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu 100 105 110

Ser Leu Val Glu Lys Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr 115 120 125

His Ser Leu Lys Thr Met Ala Asp His Arg Val Arg Ala Gly Met Ser 130 135 140

Asp Ile Arg Leu Ile Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp 145 150 150 160

Ser Phe Leu Gly Lys Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala 165 170 175

Asp Ile Ser Phe Val Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val 180 185 190

Pro Ala Leu Phe His Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala 195 200 205

Leu Ile Gly Ile Gly Ser Val Arg Val Leu Val Val Asp Ser Ser Lys 210 215 220

Phe Gly Ser Ala Gly Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp 225 230 235 240

His Ile Ile Ile Asp Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu 245 250 255

Arg Asn Ser Arg Ala Gln Ile His Val Ile Asp His Asn Gly Asp Glu 260 265 270

Ile Leu Asp Thr Pro Thr Glu Glu Asp Phe 275 280

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<222> (1)..(864)

<223> RXN01891

<400> 197

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tac aac aag gat ctg tgg gct aag gct ggc ctg gaa gat cgt ggc cca 96
Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro

gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa gcg 144 Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala

atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac ctt 192 Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr Leu

tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac tct 240 Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr Ser 65 70 75 80

gaa ggt tgg gag tcc cgt ctg act acc cca gag acc atc cgt gca gtt 288 Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala Val 85 90 95

gag tgg ctc aag tcc acc gtt gat gaa ggt ttc gca acc gtc tcc acc 336 Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser Thr 100 105 110

gac gtc acc aac gag ttc gca acc ggc ctg atc ggt tca tgc atc cag 384 Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile Gln 115 120 125

tcc acc ggt gat ctg tct tcg gtt gcc ggc gct gca agc ttc gac tgg 432 Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp Trp 130 135 140

ggc gta gca gca ctt cct aac cca acc ggc gag ggc gct tgc cca acc
Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro Thr
145 150 155 160

ggt ggc gca ggc ctg gga atc cca tct ggc atc tct gag cag cgt cag 528 Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg Gln

			165					170					175		
gac aac Asp Asn	_	_	_			-					_				576
ggc tac Gly Tyr			_					_		_	_	_	_	_	624
gca tct Ala Ser 210															672
aac gtt Asn Val 225	_			_			_		_		_	_			720
cgc gtg Arg Val	_	_				_	_				-	_	_		768
aag atc Lys Ile	_	_			_	_		_	_		_	-		_	816
gag acc Glu Thr	_	_						_	_		_				864
taatccg	agc a	actto	cagct	a ca	ac										887
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35

115 120 125 Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp Trp 135 Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro Thr 145 150 155 Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg Gln 170 Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn Thr 185 Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp Ala Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala Tyr 215 Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn Phe 230 235 Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu Glu Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu Val 265 Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu Ile 275 280 <210> 199 <211> 842 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(819) <223> FRXA01891 <400> 199 tac tac aac aag gat ctg tgg gct aag gct ggc ctg gaa gat cgt ggc 48 Tyr Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly cca gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa Pro Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu 20 25 gcg atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac 144 Ala Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr

40

ctt tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac

Leu Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr

192

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						acc Thr								288
	-	_			_	ttc Phe	_		 _			_		336
						tct Ser								384
		_	_	_		cct Pro 135					 _	_		432
						gga Gly								480
_	_		_	_	_	ttc Phe								528
						gag Glu								576
_	_		_		_	cac His	_	_					_	624
		-	-			cag Gln 215								672
						aac Asn								720
	-		_	_		ggt Gly	_	-	_	_	_	-		768
-			_	_		acc Thr			-	-	_			816
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<400> 200

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Pro Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu
20 25 30

Ala Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr 35 40 45

Leu Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr 50 55 60

Ser Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala 65 70 75 80

Val Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser 85 90 95

Thr Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile
100 105 110

Gln Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp 115 120 125

Trp Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro 130 135 140

Thr Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg 145 150 155 160

Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn 165 170 175

Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp 180 185 190

Ala Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala 195 200 205

Tyr Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn 210 215 220

Phe Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu 225 230 235 240

Glu Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu

Val Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu 260 265 270

Ile

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Gly Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro
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Asp Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr
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ggt ctt acc atc gcc atc ggt tat gta gtg gtg att tgg gcg gtg cat
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Gly Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His
ttg gca tcc atc gtc att gcg ctg ctc act ggc ttc aac ctg acc aac
                                                                   243
Leu Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn
ttt ggt att cat ccg ctg gat acc agt gca ctg tgg ggt att ttc acc
                                                                   291
Phe Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr
tca ccg ctg ttg cat gga agc ttc agc cac ctc att gga aat acc gtt
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Ser Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val
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cca ggc ttt ata ttc agt ttc ctc atc ggt atg agt ggc aag cgc gtg
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Phe Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr
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Trp Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu
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Gly Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln
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200

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Ala 65	Ser	Ile	Val	Ile	Ala 70	Leu	Leu	Thr	Gly	Phe 75	Asn	Leu	Thr	Asn	Phe 80
Gly	Ile	His	Pro	Leu 85	Asp	Thr	Ser	Ala	Leu 90	Trp	Gly	Ile	Phe	Thr 95	Ser
Pro	Leu	Leu	His 100	Gly	Ser	Phe	Ser	His 105	Leu	Ile	Gly	Asn	Thr 110	Val	Pro
Gly	Phe	Ile 115	Phe	Ser	Phe	Leu	Ile 120	Gly	Met	Ser	Gly	Lys 125	Arg	Val	Phe
Trp	Glu 130	Val	Thr	Ile	Ile	Ala 135	Gly	Leu	Ile	Gly	Gly 140	Leu	Gly	Thr	Trp
Ile 145	Phe	Gly	Gly	Ile	Gly 150	Thr	Asn	His	Ile	Gly 155	Ala	Ser	Gly	Leu	Ile 160
Tyr	Gly	Trp	Leu	Gly 165	Tyr	Leu	Ile	Val	Arg 170	Gly	Ile	Phe	Asn	Lys 175	Asp
Ile	Lys	Gln	Phe 180	Leu	Leu	Gly	Ile	Val 185	Leu	Ala	Phe	Ile	Tyr 190	Ser	Gly
Leu	Phe	Trp 195	Gly	Leu	Leu	Pro	Thr 200	Gln	Ile	Gly	Val	Ser 205	Trp	Gln	Gly
His	Leu	Phe	Gly	Ala	Leu	Gly	Gly	Ile	Gly	Ala	Gly	Ala	Phe	Ile	Ala

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gca cta aac gtg gcg tca att gct gat cta cat acc aag gga atc aag Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His Thr Lys Gly Ile Lys 185 190 195	691
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caa gct ggc gtt gat tac gcc act gtt agc gat ccc tct cgt ttc ctc Gln Ala Gly Val Asp Tyr Ala Thr Val Ser Asp Pro Ser Arg Phe Leu 215 220 225	787
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Arg Leu Pro Glu Ala Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp Asp Leu Arg Ile Leu Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile Leu Pro Ser Trp Lys Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His 185 Thr Lys Gly Ile Lys Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala 195 200 205 Phe Gly Ile Ala Gln Gln Ala Gly Val Asp Tyr Ala Thr Val Ser Asp 215 Pro Ser Arg Phe Leu Ala Pro Ser Pro Ala Gly Glu Leu His Trp 230 235 <210> 205 <211> 1314 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1291) <223> RXA01436 <400> 205 gcctaaacaa accagtcaac qacctttccc gtggcgcaac agtccctgac atcgtcaaca 60 cagtagecat cacageaatt caggeaggag gacgeageta atg gea ttg gea ett 115 Met Ala Leu Ala Leu 1 gtt ttg aac tcc ggt tca tct tcc atc aaa ttc cag ctg gtc aac ccc 163 Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe Gln Leu Val Asn Pro 10 gaa aac tot goo ato gao gag coa tat gtt tot ggt ott gtg gag cag 211 Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser Gly Leu Val Glu Gln 30 att ggt gag cca aac ggc cgc atc gta ctc aaa ata gag ggt gaa aaa 259 Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys Ile Glu Gly Glu Lys 45 tat acc cta gag aca ccc atc gca gat cac tcc gaa ggc cta aac ctg 307 Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser Glu Gly Leu Asn Leu gcg ttc gat ctc atg gac cag cac aac tgt ggt cct tcc caa ctg gaa 355 Ala Phe Asp Leu Met Asp Gln His Asn Cys Gly Pro Ser Gln Leu Glu ate ace gea gtt gga cae ege gtg gte cae gge gga ate ttg tte tee 403 Ile Thr Ala Val Gly His Arg Val Val His Gly Gly Ile Leu Phe Ser 90 95

gca ccg gaa ctt atc act gat gaa atc gtg gaa atg atc cgc gat ctc

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_	-	_					gat Asp	-			_	_	_		-	547
							cca Pro		_	_		_		_		595
							cac His									643
							tcc Ser	_	_			_		_	_	691
_			-	-			acc Thr 205					_				739
							ggt Gly									787
							ctt Leu									835
							cac His									883
														200		
	_			_		_	ctg Leu		aaa	_	-		_	aag		931
Ile	Asp	Glu ggt	Ile 265 gtt	Asp	Asn gat	Leu	_	Asn 270 gaa	aaa Lys ctg	Lys	Ser	Gly	Val 275 atc	aag Lys gac	Gly	931 979
Ile ctt Leu aat	Asp tcc Ser	Glu ggt Gly 280 caa	Ile 265 gtt Val gat	Asp aat Asn gcc	Asn gat Asp	ttc Phe	Leu cgt Arg	Asn 270 gaa Glu tac	aaa Lys ctg Leu	Lys cgg Arg	Ser gaa Glu tac	Gly atg Met 290 ata	Val 275 atc Ile cac	aag Lys gac Asp	Gly aac Asn	
ctt Leu aat Asn	Asp tcc ser gat Asp 295	Glu ggt Gly 280 caa Gln tac	Ile 265 gtt Val gat Asp	Asp aat Asn gcc Ala	Asn gat Asp tgg Trp	ttc Phe tcc Ser 300	cgt Arg 285	Asn 270 gaa Glu tac Tyr	aaa Lys ctg Leu aac Asn	Lys cgg Arg att Ile ctg	gaa Glu tac Tyr 305	Gly atg Met 290 ata Ile	Val 275 atc Ile cac His	aag Lys gac Asp caa Gln	Gly aac Asn ctc Leu acc	979
ctt Leu aat Asn cgc Arg 310	Asp tcc ser gat Asp 295 cgc Arg	Glu ggt Gly 280 caa Gln tac Tyr	Ile 265 gtt Val gat Asp ctc Leu	Asp aat Asn gcc Ala ggt Gly	Asn gat Asp tgg Trp tcc Ser 315	ttc Phe tcc Ser 300 tac Tyr	cgt Arg 285 gcg Ala	Asn 270 gaa Glu tac Tyr gtg Val	aaa Lys Ctg Leu aac Asn gca Ala	Lys cgg Arg att Ile ctg Leu 320 gcc	gaa Glu tac Tyr 305 gga Gly	Gly atg Met 290 ata Ile cgg Arg	Val 275 atc Ile cac His gta Val	aag Lys gac Asp caa Gln gac Asp	aac Asn ctc Leu acc Thr 325	979 1027

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Thr	Ala	Gly	Met 260	Ser	Ile	Asp	Glu	Ile 265	Asp	Asn	Leu	Leu	Asn 270	Lys	Lys	
Ser	Gly	Val 275	Lys	Gly	Leu	Ser	Gly 280	Val	Asn	Asp	Phe	Arg 285	Glu	Leu	Arg	
Glu	Met 290	Ile	Asp	Asn	Asn	Asp 295	Gln	Asp	Ala	Trp	Ser 300	Ala	Tyr	Asn	Ile	
Tyr 305	Ile	His	Gln	Leu	Arg 310	Arg	Tyr	Leu	Gly	Ser 315	Tyr	Met	Val	Ala	Leu 320	
Gly	Arg	Val	Asp	Thr 325	Ile	Val	Phe	Thr	Ala 330	Gly	Val	Gly	Glu	Asn 335	Ala	
Gln	Phe	Val	Arg 340	Glu	Asp	Ala	Leu	Ala 345	Gly	Leu	Glu	Met	Tyr 350	Gly	Ile	
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Ile	Ser 370	Thr	Asp	Ala	Ser	Lys 375	Val	Lys	Val	Phe	Val 380	Ile	Pro	Thr	Asn	
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ttca	atcg	gag t	gcca	aggg	ga ad	cttaç	gagga	a gca	attaa	aata				gga Gly		115
					aca Thr											163
					atg Met											211

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-				-	aaa Lys 155	_				-	-				-	595
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					caa Gln											691
					atc Ile											739
					ttg Leu											787
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Thr Glu Ile Ala Glu Leu Ala Asp Leu Pro Pro Ser Thr His Arg 35 40 45

Leu Val Ser Glu Leu Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp 50 55 60

Gly Arg Tyr Gln Leu Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr 65 70 75 80

Gly Arg Gln Leu Arg Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr 85 90 95

Ser Leu Thr Ser Glu Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu 100 105 110

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Ala Arg Val Gly Gly Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys 130 135 140

Ile Leu Leu Ala Phe Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys 145 150 155 160

Leu Pro Leu Asn Ala Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val
165 170 175

Leu Ala Ala Gln Leu Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr 180 185 190

His Asp Glu Gln Arg Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp 195 200 205

His Thr Gly Lys Leu Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala 210 215 220

Gln Ala Ala Asn Leu Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser 225 230 235 240

Gln Arg Ile Thr Lys Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu 245 250 255

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				a ttc ggt cat s Phe Gly His		163
	· -	-		g cca cac cag y Pro His Gln 35	J	211
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				a ggt gaa cac o Gly Glu His O	, , ,	355
				c tgg tca gcg u Trp Ser Ala		403
	_			t cag tgc aac r Gln Cys Asn 115		451
	Gly Tyr			c ggc cag tac e Gly Gln Tyr 130	, ,	499
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_	_				ttc Phe			_		_					931
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Pro His Gln Ala Leu Val Lys Val Leu Thr Ser Gly Ile Cys His Thr 35

Asp Leu His Ala Leu Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro

Phe Val Pro Gly His Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro

80 65 70 75 Gly Glu His Asp Val Lys Val Gly Asp Ile Val Gly Asn Ala Trp Leu 85 Trp Ser Ala Cys Gly Thr Cys Glu Tyr Cys Ile Thr Gly Arg Glu Thr 105 Gln Cys Asn Glu Ala Glu Tyr Gly Gly Tyr Thr Gln Asn Gly Ser Phe 120 Gly Gln Tyr Met Leu Val Asp Thr Arg Tyr Ala Ala Arg Ile Pro Asp 130 135 Gly Val Asp Tyr Leu Glu Ala Ala Pro Ile Leu Cys Ala Gly Val Thr Val Tyr Lys Ala Leu Lys Val Ser Glu Thr Arg Pro Gly Gln Phe Met Val Ile Ser Gly Val Gly Gly Leu Gly His Ile Ala Val Gln Tyr Ala Ala Ala Met Gly Met Arg Val Ile Ala Val Asp Ile Ala Asp Asp Lys Leu Glu Leu Ala Arg Lys His Gly Ala Glu Phe Thr Val Asn Ala Arg Asn Glu Asp Ser Gly Glu Ala Val Gln Lys Tyr Thr Asn Gly Gly Ala 230 His Gly Val Leu Val Thr Ala Val His Glu Ala Ala Phe Gly Gln Ala 250 Leu Asp Met Ala Arg Arg Ala Gly Thr Ile Val Phe Asn Gly Leu Pro Pro Gly Glu Phe Pro Ala Ser Val Phe Asn Ile Val Phe Lys Gly Leu 280 Thr Ile Arg Gly Ser Leu Val Gly Thr Arg Gln Asp Leu Ala Glu Ala 295 Leu Asp Phe Phe Ala Arg Gly Leu Ile Lys Pro Thr Val Ser Glu Cys Ser Leu Asp Glu Val Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys 330 Ile Asp Gly Arg Val Ala Ile Arg Phe 340

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Arg Thr Leu Ala Thr Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly 35 40 45

Glu Phe Asp Phe Ile Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp 50 55 60

Lys Tyr Leu Ser Leu Leu Lys Pro His Gly Val Met Ala Val Val Gly 65 70 75 80

Leu Pro Pro Glu Lys Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly
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Gly Lys Val Leu Thr Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln
100 105 110

Glu Met Leu Asp Phe Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu 115 120 125

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- cac act gtt ttt cct gtt acc cct ggt cat gag att gca gga acc atc 307 His Thr Val Phe Pro Val Thr Pro Gly His Glu Ile Ala Gly Thr Ile 55 60 65
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Gln Leu Thr Ile Ile Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala 260 265 270

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- aac tac att ggt ggc aag tgg gtt cca ccg gta gag ggc cag tac ctt 211
 Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val Glu Gly Gln Tyr Leu
- gag aac att tca cct gtc act ggt gaa gtt ttc tgt gag gtc gca cgt 259 Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe Cys Glu Val Ala Arg 40 45 50
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- cac cgc att gcg gac cgc atg gaa gag cac ctg gaa gaa atc gca gtt 403 His Arg Ile Ala Asp Arg Met Glu Glu His Leu Glu Glu Ile Ala Val 90 95 100

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- 309 -

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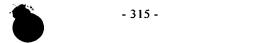
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Ser Ser Pro Asp Thr Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg 50 55 60

Glu Arg Val Glu Ser Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg 65 70 75 80

Ile Thr Val Gly Gly Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe 85 90 95

Val Glu Pro Thr Val Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala 100 105 110

Gln Asp Glu Ile Phe Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp 115 120 125

Asp Glu His Ala Ile Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly 130 135 140

Gly Thr Val Trp Thr Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg 145 150 155 160

Arg Val His Thr Gly Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro 165 170 175

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tea ace aac gtg gga ege ate etg gte ege eaa tee geg gae ega etg 192





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	cgc Arg															336
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Leu Arg Thr Ser Met Glu Leu Gly Gly Asn Ala Ala Phe Val Ile Asp 65 70 75 80

Glu Ala Ala Asp Leu Asp Glu Ala Val Ser Gly Ala Ile Ala Ala Lys 85 90 95

Leu Arg Asn Ala Gly Gln Val Cys Ile Ala Ala Asn Arg Phe Leu Val
100 105 110

His Glu Ser Arg Ala Ala Glu Phe Thr Ser Lys Leu Ala Thr Ala Met 115 120 125

Gln Asn Thr Pro Ile Gly Pro Val Ile Ser Ala Arg Gln Arg Asp Arg 130 135 140

Ile Ala Ala Leu Val Asp Glu Ala Ile Thr Asp Gly Ala Arg Leu Ile 145 150 155 160

Ile Gly Gly Glu Val Pro Asp Gly Ser Gly Phe Phe Tyr Pro Ala Thr
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Phe Gly Pro Val Ala Thr Ile Ala Thr Phe Thr Asp Leu Ala Glu Gly 195 200 205

Val Ala Gln Ala Asn Ser Thr Glu Phe Gly Leu Ala Ala Tyr Gly Phe 210 215 220

Ser Asn Asn Val Lys Ala Thr Gln Tyr Met Ala Glu His Leu Glu Ala 225 230 235 240

Gly Met Val Gly Ile Asn Arg Gly Ala Ile Ser Asp Pro Ala Ala Pro 245 250 255

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gct ggc ggt atc ggt att aat gat ggc tac gcc gcg acg tgg gcc Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala Ala Thr Trp Ala 440 445 450	
gtg tcc acg cct ctg ggt ggc atg aag cag tcg ggg ctg ggg cac Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser Gly Leu Gly His 455 460 465	
cat ggt gcg gag gga att aca aaa tat gcg gag atc cga aac atc His Gly Ala Glu Gly Ile Thr Lys Tyr Ala Glu Ile Arg Asn Ile 470 475 480	
gag cag cgc tgg atg tct atg cgt ggg ccg gcc aaa atg ccg cga Glu Gln Arg Trp Met Ser Met Arg Gly Pro Ala Lys Met Pro Arg 490 495 500	Lys
gtg tac tca gac acc gtg gcc aca gcg cta aag ctg ggc aaa atc Val Tyr Ser Asp Thr Val Ala Thr Ala Leu Lys Leu Gly Lys Ile 505 510 515	
aaa gtt ttg ccg tagcaaaaag ccggaccctt gct Lys Val Leu Pro 520	1686
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<212> PRT <213> Corynebacterium glutamicum <400> 226 Met Ile Lys Arg Leu Pro Leu Gly Pro Leu Pro Lys Glu Leu His 1 5 10 15 Thr Leu Leu Asp Leu Thr Ala Asn Ala Gln Asp Ala Ala Lys Val	Glu
<pre><212> PRT <213> Corynebacterium glutamicum <400> 226 Met Ile Lys Arg Leu Pro Leu Gly Pro Leu Pro Lys Glu Leu His</pre>	Glu
<pre><212> PRT <213> Corynebacterium glutamicum <400> 226 Met Ile Lys Arg Leu Pro Leu Gly Pro Leu Pro Lys Glu Leu His</pre>	Glu Gly Gln
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450

Asn Thr Gln Gln Tyr Val Pro Lys Gly Val Val Gly Gln Ile Thr Pro 145 150 155 Trp Asn Tyr Pro Leu Thr Leu Gly Val Ser Asp Ala Val Pro Ala Leu Leu Ala Gly Asn Ala Val Val Ala Lys Pro Asp Leu Ala Thr Pro Phe 185 Ser Cys Leu Ile Met Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg Asp Leu Met Gln Val Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala Ile Ala Ala Gln Cys Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr 235 Gly Arg Ile Leu Gly Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser Ala Glu Leu Gly Gly Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp 265 Leu Asp Lys Val Glu Ala Glu Leu Pro Gln Ala Cys Phe Ser Asn Ser 280 Gly Gln Leu Cys Val Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val 295 Tyr Glu Glu Val Ile Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser 315 Ile Gly Ala Gly Phe Glu Trp Lys Tyr Glu Met Gly Ser Leu Ile Asn His Ala Gln Leu Asp Arg Val Ser Thr Phe Val Asp Gln Ala Lys Ala 345 Ala Gly Ala Thr Val Leu Cys Gly Gly Lys Ser Arg Pro Asp Ile Gly Pro Phe Phe Tyr Glu Pro Thr Val Leu Ala Asp Val Pro Glu Gly Thr Pro Leu Leu Thr Glu Glu Val Phe Gly Pro Val Val Phe Ile Glu Lys Val Ala Thr Leu Glu Glu Ala Val Asp Lys Ala Asn Gly Thr Pro Tyr 405 410 Gly Leu Asn Ala Ser Val Phe Gly Ser Ser Glu Thr Gly Asn Leu Val 425 420 Ala Gly Gln Leu Glu Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala 440 Ala Thr Trp Ala Ser Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser

Gly Leu Gly His Arg His Gly Ala Glu Gly Ile Thr Lys Tyr Ala Glu 475 Ile Arg Asn Ile Ala Glu Gln Arg Trp Met Ser Met Arg Gly Pro Ala 485 Lys Met Pro Arg Lys Val Tyr Ser Asp Thr Val Ala Thr Ala Leu Lys 505 Leu Gly Lys Ile Phe Lys Val Leu Pro 515 <210> 227 <211> 1575 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1552) <223> RXN02674 <400> 227 atcgacctct agggcagcag tgattgattt cataaaaatc acaagtttgt aactaaaggt 60 acagttggtg aagtatccac aatcaacttt aggagacctt gtg act gca aca ttt 115 Val Thr Ala Thr Phe 1 gct gga atc gac gcc acc aaa cac ctc atc gga ggt cag tgg gtg gag 163 Ala Gly Ile Asp Ala Thr Lys His Leu Ile Gly Gly Gln Trp Val Glu gga aac tcg gat cga att tcc acc aat atc aat cct tac gac gat tcc 211 Gly Asn Ser Asp Arg Ile Ser Thr Asn Ile Asn Pro Tyr Asp Asp Ser gta atc gcc gaa agc aaa caa gct tcc att gct gat gtt gat gcc gcg 259 Val Ile Ala Glu Ser Lys Gln Ala Ser Ile Ala Asp Val Asp Ala Ala tat gaa gcc gcg aag aag gcc cag gct gag tgg gca gct acg ccc gct 307 Tyr Glu Ala Ala Lys Lys Ala Gln Ala Glu Trp Ala Ala Thr Pro Ala gcg gaa cga tct gcc atc atc tac cgt gcg gct gaa ctt ctt gaa gag 355 Ala Glu Arg Ser Ala Ile Ile Tyr Arg Ala Ala Glu Leu Leu Glu Glu cac cgg gag gaa atc gtg gaa tgg ctg atc aag gaa tcc ggc tcg acg 403 His Arg Glu Glu Ile Val Glu Trp Leu Ile Lys Glu Ser Gly Ser Thr cgt tcc aag gct aat ttg gaa atc act ttg gca gga aac atc act aaa 451 Arg Ser Lys Ala Asn Leu Glu Ile Thr Leu Ala Gly Asn Ile Thr Lys 105 110 gaa tog got toa tto oot ggt ogt gtg cat ggt oga att tot oot tog 499 Glu Ser Ala Ser Phe Pro Gly Arg Val His Gly Arg Ile Ser Pro Ser

125

120

		ccg Pro			_		_			_	_	_	_		_	547
		gtg Val											_		_	595
		gct Ala														643
		gat Asp														691
		gcc Ala 200													_	739
		gaa Glu														787
		ttc Phe														835
		aat Asn														883
		ccg Pro			-		_	_	-	-		-	-	_	_	931
_	-	gcc Ala 280	_	_		-				_		_		_	_	979
		aac Asn														1027
		ttc Phe														1075
		gga Gly			_			-			-	_	_		_	1123
		aag Lys														1171
		gaa Glu 360														1219

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					gac Asp											1267
					ctg Leu 395											1315
					gac Asp											1363
_		_	_	_	gcc Ala	_		_	_	_		_				1411
-				_	ctc Leu		-		_	-				_		1459
			_		tct Ser				_				_			1507
					aca Thr 475											1552
taat	tgtt	tt t	cgad	cgtaa	ac co	cc										1575
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Arg Ile Ser Pro Ser Asn Thr Pro Gly Lys Glu Asn Arg Val Tyr Arg Val Ala Lys Gly Val Val Gly Val Ile Ser Pro Trp Asn Phe Pro Leu 150 155 Asn Leu Ser Ile Arg Ser Val Ala Pro Ala Leu Ala Val Gly Asn Ala Val Val Ile Lys Pro Ala Ser Asp Thr Pro Val Thr Gly Gly Val Ile 180 185 Pro Ala Arg Ile Phe Glu Glu Ala Gly Val Pro Ala Gly Val Ile Ser 200 Thr Val Ala Gly Ala Gly Ser Glu Ile Gly Asp His Phe Val Thr His 210 215 Ala Val Pro Lys Leu Ile Ser Phe Thr Gly Ser Thr Pro Val Gly Arg 230 235 Arg Val Gly Glu Leu Ala Ile Asn Gly Gly Pro Met Lys Thr Val Ala Leu Glu Leu Gly Gly Asn Ala Pro Phe Val Val Leu Ala Asp Ala Asp Ile Asp Ala Ala Ala Gln Ala Ala Ala Val Gly Ala Phe Leu His Gln Gly Gln Ile Cys Met Ser Ile Asn Arg Val Ile Val Asp Ala Ala Val 295 His Asp Glu Phe Leu Glu Lys Phe Val Glu Ala Val Lys Asn Ile Pro 310 315 Thr Gly Asp Pro Ser Ala Glu Gly Thr Leu Val Gly Pro Val Ile Asn 330 Asp Ser Gln Leu Ser Gly Leu Lys Glu Lys Ile Glu Leu Ala Lys Lys 345 Glu Gly Ala Thr Val Gln Val Glu Gly Pro Ile Glu Gly Arg Leu Val His Pro His Val Phe Ser Asp Val Thr Ser Asp Met Glu Ile Ala Arg 375 Glu Glu Ile Phe Gly Pro Leu Ile Ser Val Leu Lys Ala Asp Asp Glu Ala His Ala Ala Glu Leu Ala Asn Ala Ser Asp Phe Gly Leu Ser Ala Ala Val Trp Ser Lys Asp Ile Asp Arg Ala Ala Gln Phe Ala Leu Gln Ile Asp Ser Gly Met Val His Ile Asn Asp Leu Thr Val Asn Asp Glu 440 Pro His Val Met Phe Gly Gly Ser Lys Asn Ser Gly Leu Gly Arg Phe

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450 455 460

Asn Gly Asp Trp Ala Ile Glu Glu Phe Thr Thr Asp Arg Trp Ile Gly 465 470 475 480

Ile Lys Arg Ser

<210> 229

<211> 2034

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2011)

<223> RXN00868

<400> 229

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cttgccatat	gagaacgcaa	acaaggaggg	ataaaatttc	atg	gct	gaa	acg	aag	115
				Met	Ala	Glu	Thr	Lys	
				1				5	

- aga atg aca gtt agc cag gca ctg gtt gaa ttc ctt ggt cac cag tgg 163 Arg Met Thr Val Ser Gln Ala Leu Val Glu Phe Leu Gly His Gln Trp 10 15 20
- act gtc gac ggc gat atc cgc gag cgc acc att cca ggc atg ttc gga 211
 Thr Val Asp Gly Asp Ile Arg Glu Arg Thr Ile Pro Gly Met Phe Gly
 25 30 35
- att ttc gga cac gga aac gtt gct ggc att ggc cag gca ctc aag cag 259 Ile Phe Gly His Gly Asn Val Ala Gly Ile Gly Gln Ala Leu Lys Gln 40 45 50
- tac aac gtt gaa caa cct gag ctc atg ccg tac tac cag gct cgt aat 307
 Tyr Asn Val Glu Gln Pro Glu Leu Met Pro Tyr Tyr Gln Ala Arg Asn
 60
 65
- gag cag gcg atg gtg cac cag tct gtt gga tat gca cgc atg cac cgc 355 Glu Gln Ala Met Val His Gln Ser Val Gly Tyr Ala Arg Met His Arg 70 75 80 85
- cgt cgt ggc aca tac gca tct gcc gca tct gtt gga ccc ggc gcg acc 403 Arg Arg Gly Thr Tyr Ala Ser Ala Ala Ser Val Gly Pro Gly Ala Thr 90 95 100
- aac ctg tta acc ggt gcg gct ctt gct acc acc aac cgt ttg cca gcg $\,$ 451 Asn Leu Eu Thr Gly Ala Ala Leu Ala Thr Thr Asn Arg Leu Pro Ala $\,$ 105 $\,$ 110 $\,$ 115
- ttg ctg ctg cct agt gat act ttt gcc acc cgc gtg gcg gat cca gtg 499 Leu Leu Pro Ser Asp Thr Phe Ala Thr Arg Val Ala Asp Pro Val 120 125 130
- ttg cag cag ttg gag cag cca tgg gat atc ggg ctg acg gtt aat gat 547 Leu Gln Gln Leu Glu Gln Pro Trp Asp Ile Gly Leu Thr Val Asn Asp 135 140 145

					tct Ser 155											595
					gcg Ala											643
_	-			-	gtc Val			-			-	_		-	-	691
					ccg Pro											739
		_		_	cca Pro		_	_		_	-	_			_	787
					aag Lys 235											835
_			_		gaa Glu	_	_	_	_	_				_		883
					acc Thr											931
					tta Leu											979
					ggt Gly											1027
					acc Thr 315											1075
					aac Asn											1123
					cct Pro											1171
		-	_	_	ctg Leu	_					-		-			1219
					gaa Glu											1267

		_			ggt Gly 395			_			_	-				1315
					tcg Ser											1363
					ggt Gly											1411
					gtg Val											1459
					ggc Gly											1507
					atc Ile 475											1555
					acg Thr											1603
					cac His			_					_		_	1651
		_	_	_	cgt Arg						_	-		_	_	1699
					cag Gln											1747
					tac Tyr 555											1795
					gat Asp											1843
					ttc Phe											1891
					ggt Gly											1939
					aac Asn											1987
gcc	ctc	cag	cgt	ccg	ctg	ctc	ggc	taaa	ccaç	gtt <u>c</u>	ggcta	aaaco	ca aa	aa		2034

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Ala Leu Gln Arg Pro Leu Leu Gly 630 635

<210> 230

<211> 637

<212> PRT

<213> Corynebacterium glutamicum

<400> 230

Met Ala Glu Thr Lys Arg Met Thr Val Ser Gln Ala Leu Val Glu Phe $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Leu Gly His Gln Trp Thr Val Asp Gly Asp Ile Arg Glu Arg Thr Ile 20 25 30

Pro Gly Met Phe Gly Ile Phe Gly His Gly Asn Val Ala Gly Ile Gly 35 40 45

Gln Ala Leu Lys Gln Tyr Asn Val Glu Gln Pro Glu Leu Met Pro Tyr 50 55 60

Tyr Gln Ala Arg Asn Glu Gln Ala Met Val His Gln Ser Val Gly Tyr 65 70 75 80

Ala Arg Met His Arg Arg Arg Gly Thr Tyr Ala Ser Ala Ala Ser Val $85 \hspace{1.5cm} 90 \hspace{1.5cm} 95$

Gly Pro Gly Ala Thr Asn Leu Leu Thr Gly Ala Ala Leu Ala Thr Thr
100 105 110

Asn Arg Leu Pro Ala Leu Leu Pro Ser Asp Thr Phe Ala Thr Arg 115 120 125

Val Ala Asp Pro Val Leu Gln Gln Leu Glu Gln Pro Trp Asp Ile Gly 130 135 140

Leu Thr Val Asn Asp Ala Phe Arg Pro Val Ser Lys Phe Phe Asp Arg 145 150 155 160

Val Gln Arg Pro Glu Gln Leu Phe Ser Ile Ala Leu Ala Ala Met Arg 165 170 175

Val Leu Thr Asp Pro Ala Glu Thr Gly Ala Val Thr Ile Ala Leu Pro 180 185 190

Glu Asp Val Gln Ala Glu Met Leu Asp Val Pro Val Glu Phe Leu Gln 195 200 205

Asp Arg Glu Trp His Ile Arg Arg Pro Arg Pro Glu Arg Ala Ala Leu 210 215 220

Ala Arg Ala Ile Glu Val Ile Lys Asn Ala Lys Asn Pro Met Ile Ile 225 230 235 240

Ala Gly Gly Gly Val Leu Tyr Ser Asp Ala Glu Thr Gln Leu Gln Ala 245 250 255

Leu Val Glu Gln Thr Gly Ile Pro Val Gly Thr Ser Gln Ala Gly Gly 260 265 270

Gly Val Leu Ala Trp Asp His Ala Gln Asn Leu Gly Gly Val Gly Ala 275 280 285

Thr Gly Thr Leu Ala Ala Asn Arg Ile Ala Gly Asp Ala Asp Val Ile 290 295 300

Ile Gly Ile Gly Thr Arg Tyr Ser Asp Phe Thr Thr Ala Ser Arg Thr 305 310 315 320

Ala Phe Gln Asn Pro Asp Val Thr Phe Ile Asn Ile Asn Val Ala Ser 325 330 335

Phe Asp Ala Tyr Lys His Gly Thr Gln Leu Pro Val Ile Ala Asp Ala 340 345 350

Arg Glu Ala Ile Val Glu Leu Ala Glu Ala Leu Gln Gly Phe Thr Val 355 360 365

Ala Glu Asp Tyr Ala Gln Arg Ile Ala Lys Glu Lys Ala Ala Trp Asp 370 375 380

Ala Glu Val Asp Lys Ser Phe Ala Pro Ser Gly Leu Ala Leu Pro Gly 385 390 395 400

Gln Pro Glu Ile Ile Gly Ala Val Gln Ala Ser Thr Ser Glu Lys Asp 405 410 415

Val Ile Val Gln Ala Ala Gly Ser Leu Pro Gly Asp Leu His Lys Leu
420 425 430

Trp Arg Val Arg Asp Ala Leu Gly Tyr His Val Glu Tyr Ala Phe Ser 435 440 445

Cys Met Gly Tyr Glu Ile Ala Gly Gly Ile Gly Ala Lys Arg Gly Leu 450 455 460

Asp Ala Ala Gly Asp Asp Arg Asp Val Val Ile Met Val Gly Asp Gly 465 470 475 480

Ser Tyr Leu Met Leu Asn Thr Glu Leu Val Thr Ala Val Ala Glu Gly
485 490 495

Ile Lys Val Ile Val Val Leu Ile Gln Asn His Gly Tyr Ala Ser Ile 500 505 510

Gly His Leu Ser Glu Thr Val Gly Ser Gln Arg Phe Gly Thr Trp Tyr 515 520 525

Arg Glu Tyr Asp Ala Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu 530 535 540

Pro Val Asp Leu Ala Met Asn Ala Arg Ser Tyr Gly Met Asp Val Ile 545 550 555 560

Glu Val Glu Pro Ser Ala Asn Ala Ile Glu Asp Leu Lys Ala Ala Met 565 570 575

Ala Thr Ala Lys Ala Ser Glu Lys Ser Thr Phe Ile His Ile Asn Ser 580 585 590

Asp Pro Leu Ile Tyr Ala Pro Asp Gly Ala Gly Trp Trp Asp Val Pro

595 600 605 Val Ser Glu Thr Ser Thr Leu Asp Ser Thr Asn Ala Ala Arg Glu Asp 615 Tyr Leu Lys Asn Gln Ala Leu Gln Arg Pro Leu Leu Gly 630 <210> 231 <211> 1142 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(1119) <223> RXN01143 <400> 231 48 atc cca gtt gtc acc acc ttg atg gct ttg ggt act ttc cca gag tct Ile Pro Val Val Thr Thr Leu Met Ala Leu Gly Thr Phe Pro Glu Ser cac gag ctg cac atg ggt atg cca ggc atg cat ggc act gtg tcc gct 96 His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala gtt ggt gca ctg cag cgc agc gac ctg ctg att gct atc ggc tcc cgc 144 Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg 35 40 ttt gat gac cgc gtc acc ggt gac gtt gac acc ttc gcg cct gac gcc 192 Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala 50 55 aag atc att cac gcc gac att gat cct gcc gaa atc ggc aag atc aag 240 Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys 70 cag gtt gag gtt cca atc gtg ggc gat gcc cgc gaa gtt ctt gct cgt 288 Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg 85 ctg ctg gaa acc acc aag gca agc aag gca gag acc gag gac atc tcc 336 Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser gag tgg gtt gac tac ctc aag ggc ctc aag gca cgt ttc ccg cgt ggc 384 Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly 120 tac gac gag cag cca ggc gat ctg ctg gca cca cag ttt gtc att gaa 432 Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu 135 acc ctg tcc aag gaa gtt ggc ccc gac gca att tac tgc gcc ggc gtt 480 Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val 150 155 ggc cag cac caa atg tgg gca gct cag ttc gtt gac ttt gaa aag cca 528

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Gly	Gln	His	Gln	Met 165	Trp	Ala	Ala	Gln	Phe 170	Val	Asp	Phe	Glu	Lys 175	Pro	
	acc Thr															576
	gcg Ala															624
	atc Ile 210															672
	gcc Ala	_	_	-					_		_					720
	aaa Lys															768
	cgg Arg							_		_				_		816
	ttt Phe									-	_	_		_	_	864
	aaa Lys 290			_	_	_		-			_	_	_			912
	gac Asp	-		-	_		_			-		-	_	-	-	960
_	tgg Trp		-			_						_		_		1008
	ctc Leu															1056
	cct Pro															1104
	tcg Ser 370				taaç	ggaga	aga d	ccaa	agato	gg ct	a					1142

<210> 232

<211> 373

<212> PRT

<213> Corynebacterium glutamicum

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His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala 20 25 30

Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg 35 40 45

Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala 50 55 60

Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys 65 70 75 80

Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg 85 90 95

Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser 100 105 110

Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly
115 120 125

Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu 130 135 140

Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val 145 150 155 160

Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro 165 170 175

Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly Thr Met Gly Tyr Ala Val

Pro Ala Ala Leu Gly Ala Lys Ala Gly Ala Pro Asp Lys Glu Val Trp 195 200 205

Ala Ile Asp Gly Asp Gly Cys Phe Gln Met Thr Asn Gln Glu Leu Thr 210 215 220

Thr Ala Ala Val Glu Gly Phe Pro Ile Lys Ile Ala Leu Ile Asn Asn 225 230 235 240

Gly Lys Pro Gly Ala Trp Val Arg Gln Trp Gln Thr Leu Phe Tyr Glu 245 250 255

Gly Arg Tyr Ser Asn Thr Lys Leu Arg Asn Gln Gly Glu Tyr Met Pro 260 265 270

Asp Phe Val Thr Leu Ser Glu Gly Leu Gly Cys Val Ala Ile Arg Val 275 280 285

Thr Lys Ala Glu Glu Val Leu Pro Ala Ile Gln Lys Ala Arg Glu Ile 290 295 300

Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val Gly Glu Asp Ala Gln 305 310 315 320 Val Trp Pro Met Val Ser Ala Gly Ser Ser Asn Ser Asp Ile Gln Tyr Ala Leu Gly Leu Arg Pro Phe Phe Asp Gly Asp Glu Ser Ala Ala Glu Asp Pro Ala Asp Ile His Glu Ala Val Ser Asp Ile Asp Ala Ala Val Glu Ser Thr Glu Ala 370 <210> 233 <211> 793 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(793) <223> RXN01146 <400> 233 tatttagtaa aggagccaga aagtcgtgaa tgtggcagct tctcaacagc ccactcccgc 60 cacggttgca agccgtggtc gatccgccgc ccctgagcgg atg aca ggt gca aag 115 Met Thr Gly Ala Lys gca att gtt cga tcg ctc gag gag ctt aac gcc gac atc gtg ttc ggt 163 Ala Ile Val Arg Ser Leu Glu Glu Leu Asn Ala Asp Ile Val Phe Gly att cct ggt ggt gcg gtg cta ccg gtg tat gac ccg ctc tat tcc tcc 211 Ile Pro Gly Gly Ala Val Leu Pro Val Tyr Asp Pro Leu Tyr Ser Ser aca aag gtg cgc cac gtc ttg gtg cgc cac gag cag ggc gca ggc cac 259 Thr Lys Val Arg His Val Leu Val Arg His Glu Gln Gly Ala Gly His gca gca acc ggc tac gcg cag gtt act gga cgc gtt ggc gtc tgc att 307 Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Arg Val Gly Val Cys Ile gca acc tct ggc cca gga gca acc aac ttg gtt acc cca atc gct gat 355 Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val Thr Pro Ile Ala Asp gca aac ttg gac tcc gtt ccc atg gtt gcc atc acc ggc cag gtc gga 403 Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile Thr Gly Gln Val Gly agt ggc ctg ctg ggt acc gac gct ttc cag gaa gcc gat atc cgc ggc 451 Ser Gly Leu Leu Gly Thr Asp Ala Phe Gln Glu Ala Asp Ile Arg Gly 110

ate ace atg cca gtg ace aag cac aac tte atg gte ace aac eet aac

Ile Thr Met Pro Val Thr Lys His Asn Phe Met Val Thr Asn Pro Asn

125

120

499

gac att cca cag gca ttg gct gag gca ttc cac ctc gcg att act Asp Ile Pro Gln Ala Leu Ala Glu Ala Phe His Leu Ala Ile Thr 135 140 145	
cgc cct ggc cct gtt ctg gtg gat att cct aag gat gtc cag aac Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys Asp Val Gln Asn 150 155 160	
gaa ttg gat ttc gtc tgg cca cca aag atc gac ctg cca ggc tac Glu Leu Asp Phe Val Trp Pro Pro Lys Ile Asp Leu Pro Gly Tyr 170 175 180	_
cca gtt tca aca cca cat gct cgc cag atc gag cag gca gtc aag Pro Val Ser Thr Pro His Ala Arg Gln Ile Glu Gln Ala Val Lys 185 190 195	-
atc ggt gag gcc aag aag ccc gtc ctt tac gtt ggt ggc gta Ile Gly Glu Ala Lys Lys Pro Val Leu Tyr Val Gly Gly Val 200 205 210	
aag gct gac gca cac gaa gag ctt cgt gcg ttc gct gag tac acc Lys Ala Asp Ala His Glu Glu Leu Arg Ala Phe Ala Glu Tyr Thr 215 220 225	
atc cca Ile Pro 230	793
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<212> PRT <213> Corynebacterium glutamicum <400> 234 Met Thr Gly Ala Lys Ala Ile Val Arg Ser Leu Glu Glu Leu Asn 1 5 10 15 Asp Ile Val Phe Gly Ile Pro Gly Gly Ala Val Leu Pro Val Tyr	Asp
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135 140 130 Leu Ala Ile Thr Gly Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys 155 Asp Val Gln Asn Ala Glu Leu Asp Phe Val Trp Pro Pro Lys Ile Asp 165 Leu Pro Gly Tyr Arg Pro Val Ser Thr Pro His Ala Arg Gln Ile Glu 185 Gln Ala Val Lys Leu Ile Gly Glu Ala Lys Lys Pro Val Leu Tyr Val 195 Gly Gly Val Ile Lys Ala Asp Ala His Glu Glu Leu Arg Ala Phe 215 Ala Glu Tyr Thr Gly Ile Pro 230 <210> 235 <211> 639 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(616) <223> RXN01144 <400> 235 ggtgatgaat ctgcagcaga agatcctgcc gacattcacg aagccgtcag cgacattgat 60 gccgccgttg aatcgaccga ggcataagga gagacccaag atg gct aat tet gac 115 Met Ala Asn Ser Asp gtc acc cgc cac atc ctg tcc gta ctc gtt cag gac gta gac gga atc 163 Val Thr Arg His Ile Leu Ser Val Leu Val Gln Asp Val Asp Gly Ile att tee ege gta tea ggt atg tte ace ega ege gea tte aac ete gtg 211 Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg Ala Phe Asn Leu Val 259 ttc ctc gtg tct gca aag acc gaa aca cac ggc atc aac cgc atc acg Phe Leu Val Ser Ala Lys Thr Glu Thr His Gly Ile Asn Arg Ile Thr gtt gtt gtc gac gcc gac gag ctc aac att gag cag atc acc aag cag 307 Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu Gln Ile Thr Lys Gln ctc aac aag ctg atc ccc gtg ctc aaa gtc gtg cga ctt gat gaa gag 355 Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val Arg Leu Asp Glu Glu 75 acc act atc gcc cgc gca atc atg ctg gtt aag gtc tct gcg gac agc 403 Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys Val Ser Ala Asp Ser 95

		_	_	_		gtc Val	_	-					_	_	cga Arg	451
-	-	-	-	_		gac Asp			_		-					499
		_		_	_	ctg Leu 140		_		_	_					547
_	_	_			Ser	gga Gly	Gln	Ile	_			_		_	_	595
					aag Lys	atc Ile	taaa	acago	caa t	taat	ctga	at to	gc			639

<210> 236

<211> 172

<212> PRT

<213> Corynebacterium glutamicum

<400> 236

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Asp Val Asp Gly Ile Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg 20 25 30

Ala Phe Asn Leu Val Phe Leu Val Ser Ala Lys Thr Glu Thr His Gly 35 40 45

Ile Asn Arg Ile Thr Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu 50 60

Gln Ile Thr Lys Gln Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val 65 70 75 80

Arg Leu Asp Glu Glu Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys 85 90 95

Val Ser Ala Asp Ser Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn 100 105 110

Ile Phe Arg Ala Arg Val Val Asp Val Ala Pro Asp Ser Val Val Ile
115 120 125

Glu Ser Thr Gly Thr Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met 130 135 140

Glu Pro Phe Gly Ile Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu 145 150 155 160

Asn Arg Gly Pro Lys Thr Met Ala Pro Ala Lys Ile 165 170

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aatcttgaga atttattttg aggaagcaag aggaagtgtc atg agc aaa gtt gca
                                            Met Ser Lys Val Ala
atg gtt acc ggt ggt gca caa ggc atc ggt cgt gga att tca gag aag
                                                                   163
Met Val Thr Gly Gly Ala Gln Gly Ile Gly Arg Gly Ile Ser Glu Lys
ctg gca gca gat ggt ttc gat att gcc gta gcc gac ctg cca caa cag
                                                                   211
Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala Asp Leu Pro Gln Gln
             25
gaa gaa caa gct gca gag acc atc aag ttg att gaa gct gca ggt caa
                                                                   259
Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile Glu Ala Ala Gly Gln
aag gct gta ttc gtt gga tta gat gtc acc gat aag gct aat ttc gac
                                                                   307
Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp Lys Ala Asn Phe Asp
                                                                   355
agt gca att gat gag gca gca gag aaa ctt ggc ggc ttc gat gtg cta
Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly Gly Phe Asp Val Leu
gta aac aac gcc ggc atc gca caa att aag cca ctt ctg gaa gtc acc
                                                                   403
Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro Leu Leu Glu Val Thr
                 90
gaa gaa gac cta aag cag atc tac tcc gtg aac gtt ttt agc gta ttt
                                                                   451
Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn Val Phe Ser Val Phe
                                110
ttt ggt att caa gca gca tcc cga aag ttc gat gag ctt ggc gta aaa
                                                                   499
Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp Glu Leu Gly Val Lys
        120
ggc aag atc atc aac gct gca tca atc gct gct atc caa ggt ttc cca
                                                                   547
Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala Ile Gln Gly Phe Pro
                        140
atc ttg agc gcc tac tcc acc aca atc gcg gtt cgt ggc ctc acc
                                                                   595
Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala Val Arg Gly Leu Thr
                    155
cag gct gct gcg caa gaa ctc gca ccc aag ggt cac acc gtg aat gcc
                                                                   643
Gln Ala Ala Gln Glu Leu Ala Pro Lys Gly His Thr Val Asn Ala
                170
                                    175
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							acc Thr										691
-			_				aag Lys 205							_			739
					-	_	ggc Gly	-			-			-	_		787
							gct Ala										835
	_	_	_		_	_	ggc Gly		_				tag	gggtt	:gc		884
tttc	ccgc	cac t	ca														897
<211 <212)> 23 l> 25 2> PF B> Co	58 RT	ebact	ceri	ım gl	Lutar	nicur	n									
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Gly	Ile	Ser	Glu 20	Lys	Leu	Ala	Ala	Asp 25	Gly	Phe	Asp	Ile	Ala 30	Val	Ala		
Asp	Leu	Pro 35	Gln	Gln	Glu	Glu	Gln 40	Ala	Ala	Glu	Thr	Ile 45	Lys	Leu	Ile		
Glu	Ala 50	Ala	Gly	Gln	Lys	Ala 55	Val	Phe	Val -	Gly	Leu 60	Asp	Val	Thr	Asp		
Lys 65	Ala	Asn	Phe	Asp	Ser 70	Ala	Ile	Asp	Glu	Ala 75	Ala	Glu	Lys	Leu	Gly 80	,	
Gly	Phe	Asp	Val	Leu 85	Val	Asn	Asn	Ala	Gly 90	Ile	Ala	Gln	Ile	Lys 95	Pro		
Leu	Leu	Glu	Val 100	Thr	Glu	Glu	Asp	Leu 105	Lys	Gln	Ile	Tyr	Ser 110	Val	Asn		
Val	Phe	Ser 115	Val	Phe	Phe	Gly	Ile 120	Gln	Ala	Ala	Ser	Arg 125	Lys	Phe	Asp		
Glu	Leu 130	Gly	Val	Lys	Gly	Lys 135	Ile	Ile	Asn	Ala	Ala 140	Ser	Ile	Ala	Ala		
Ile 145	Gln	Gly	Phe	Pro	Ile 150	Leu	Ser	Ala	Tyr	Ser 155	Thr	Thr	Lys	Phe	Ala 160		
Val	Arg	Gly	Leu	Thr	Gln	Ala	Ala	Ala	Gln	Glu	Leu	Ala	Pro	Lys	Gly		

.

165 170 His Thr Val Asn Ala Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp 185 Glu Gln Ile Asp Ala Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly Glu Asn Phe Lys Glu Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser 215 Val Pro Glu Asp Val Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn 225 230 235 Ser Asn Tyr Ile Thr Gly Gln Val Met Leu Val Asp Gly Gly Met Leu 245 250 Tyr Asn <210> 239 <211> 876 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(853) <223> RXA02453 <400> 239 aaccaacaaa ggtcatctca accggcttaa gaaaattctg ccagctttct gctgattgaa 60 tegtgecage teagggeata teteacetaa agtaaacace atg aaa tea ate tte 115 Met Lys Ser Ile Phe att too ggt gcg gcg aac gga att ggc aaa gct gtg gcg ttg aaa ttt 163 Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala Val Ala Leu Lys Phe ctt cac gaa ggt tgg ctc gtt gga gcc tac gac ctc gcg gaa atc acc 211 Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp Leu Ala Glu Ile Thr 25 tac tea cac eec aat ett ege tgg gge tac etc aat gtt ega eag tee 259 Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu Asn Val Arg Gln Ser 40 gag tog tgg gac aaa gcc cta gaa gac ttt gcg acg cac acc gga ggc 307 Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala Thr His Thr Gly Gly acc atc gat gtg gtg gac aat aat gcc ggc gta att att gag gga ccg 355 Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val Ile Ile Glu Gly Pro 75 ctg cag gac gca gag gag ggg agc gtc gac aag ctt ctt gca atc aac 403 Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys Leu Leu Ala Ile Asn 90 95

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						ggt Gly										451
						ttg Leu										499
						gcg Ala 140										547
						ctg Leu										595
					-	cct Pro										643
		_	_	-		ctg Leu	_	_	_		-				_	691
_	_		_	_		gta Val		_				_				739
		_		_		cat His 220					_		-	_		787
_			_			ctg Leu	-		_		_		_	_		835
	_	cta Leu		-		taaa	atgaa	att q	gatta	atttt	a go	jc				876

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<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

Met Lys Ser Ile Phe Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala 1 5 10 15

Val Ala Leu Lys Phe Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp $20 \hspace{1cm} 25 \hspace{1cm} 30$

Leu Ala Glu Ile Thr Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu $35 \hspace{1.5cm} 40 \hspace{1.5cm} 45$

Asn Val Arg Gln Ser Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala 50 55 60

Thr His Thr Gly Gly Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val

65					70					/5					80	
Ile	Ile	Glu	Gly	Pro 85	Leu	Gln	Asp	Ala	Glu 90	Glu	Gly	Ser	Val	Asp 95	Lys	
Leu	Leu	Ala	Ile 100	Asn	Val	Asn	Gly	Val 105	Thr	Leu	Gly	Ala	Arg 110	Ala	Ala	
His	Pro	Tyr 115	Leu	Ala	Arg	Thr	Pro 120	Gly	Ala	Gln	Leu	Leu 125	Asn	Met	Ser	
Ser	Ala 130	Ser	Ala	Val	Tyr	Gly 135	Gln	Pro	Gln	Ile	Ala 140	Val	Tyr	Ser	Ala	
Ser 145	Lys	Phe	Tyr	Val	Ala 150	Gly	Leu	Thr	Glu	Ala 155	Leu	Asn	Leu	Glu	Trp 160	
Arg	Lys	Asp	Asp	Ile 165	Arg	Val	Val	Asp	Val 170	Trp	Pro	Leu	Trp	Ala 175	Lys	
Thr	Asp	Leu	Val 180	Asn	Gly	Val	Lys	Ala 185	Lys	Ser	Leu	Lys	Arg 190	Leu	Gly	
Val	Arg	Ile 195	Thr	Pro	Glu	Gln	Val 200	Ala	Gln	Ala	Val	Trp 205	Asp	Ala	Val	
His	Pro 210	Lys	Ser	Arg	Trp	Ala 215	Lys	Gly	Lys	Val	His 220	His	Gly	Val	Ser	
Lys 225	Leu	Asp	Lys	Ala	Leu 230	Tyr	Leu	Met	Lys	Ser 235	Leu	Ser	Pro	Asp	Arg 240	
Val	Ala	Met	Cys	Phe 245	Ala	Arg	Leu	Ile	Ala 250	Gly						
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<222	.> CE ?> (1	os 101). KS017		L 1 7)												
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gata	igege	egc t	caga	agtt	c tt	tagt	gaaa	ı gca	agaad	caa			aaa Lys			115
					gaa Glu											163
					aaa Lys											211

						gat Asp										259
						acc Thr 60										307
						gta Val										355
_						ggc Gly		_		_	_	_		_	_	403
						tgc Cys										- 451
						cag Gln										499
						atg Met 140										547
-	-					ttc Phe			_	_		-	-	_	-	595
				_		gtc Val								_		643
						aaa Lys										691
						gag Glu										739
		-	_		_	ctg Leu 220				_				-		787
		_	_	_		ttg Leu						_				835
						ctt Leu										883
	_	_			_	atc Ile		-	_	_	-		_	_	_	931
aac	cgt	cag	atc	atc	aca	ggt	cac	ctc	act	gga	agt	gcg	aat	gac	acg	979

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Asn Arg Gln I	le Ile Thr	Gly His Le	eu Thr Gly Se	r Ala Asn As 290	p Thr
gaa cag act a Glu Gln Thr M 295				l Lys Pro Le	
gaa cgg atg c Glu Arg Met P 310	_	_		-	
gct ggt aaa c Ala Gly Lys P	_			-	1117
taatgccaac ag	caagccca a	tt			1140
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<400> 242 Met Pro Lys T	yr Ile Ala 5	Met Gln Va	al Ser Glu Se 10	r Gly Ala Pr 1	
Ala Ala Asn L	eu Val Gln 20		co Leu Lys Se 25	r Arg Glu Va 30	l Arg
Val Glu Ile A.	la Ala Ser	Gly Val Cy 40	ys His Ala As _l	o Ile Gly Th 45	r Ala
Ala Ala Ser G	ly Lys His	Thr Val Ph 55	ne Pro Val Th	-	s Glu
Ile Ala Gly T	nr Ile Ala 70	Glu Ile Gl	ly Glu Asn Va. 75	l Ser Arg Tr	p Thr 80
Val Gly Asp A	rg Val Ala 85	Ile Gly Tr	rp Phe Gly Gl	y Asn Cys Gl 9	
Cys Ala Phe C	ys Arg Ala 00	Gly Asp Pr		s Arg Glu Ar 110	g Lys
Ile Pro Gly V	al Ser Tyr	Ala Gly Gl 120	ly Trp Ala Gl	n Asn Ile Va 125	l Val
Pro Ala Glu A. 130	la Leu Ala	Ala Ile Pr 135	co Asp Gly Me		r Glu
Pro Ala Pro Mo 145	et Gly Cys 150	Ala Gly Va	al Thr Thr Pho 155	e Asn Ala Le	u Arg 160
Asn Leu Lys L	eu Asp Pro 165	Gly Ala Al	la Val Ala Va 170	l Phe Gly Il 17	_
Gly Leu Val A	g Leu Ala 30	Ile Gln Ph	_	s Met Gly Ty 190	r Arg
Thr Ile Thr I	le Ala Arg	Gly Leu Gl	iu Arg Glu Gli	ı Leu Ala Ar	g Gln

195 200 205 Leu Gly Ala Asn His Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln 215 Ala Leu Phe Glu Leu Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser 225 230 235 Thr Thr Glu Pro Leu Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly 250 Gln Leu Thr Ile Ile Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala 260 265 Ala Gln Leu Met Met Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly 280 Ser Ala Asn Asp Thr Glu Gln Thr Met Lys Phe Ala His Leu His Gly Val Lys Pro Leu Ile Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala Ile Ala Arg Ile Ser Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu 330 Pro Asn Ser <210> 243 <211> 1665 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1642) <223> RXA02737 <400> 243 agcacgctgc atcagtaacg gcgacatgaa atcgaattag ttcgatctta tgtggccgtt 60 acacatettt cattaaagaa aggategtga cactaceate gtg age aca aac aeg 115 Val Ser Thr Asn Thr ace eee tee age tgg aca aac eea etg ege gae eeg eag gat aaa ega 163 Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp Pro Gln Asp Lys Arg 10 ctc ccc cgc atc gct ggc cct tcc ggc atg gtg atc ttc ggt gtc act Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val Ile Phe Gly Val Thr 25 30 ggc gac ttg gct cga aag aag ctg ctc ccc gcc att tat gat cta gca 259 Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala Ile Tyr Asp Leu Ala 40 45 50 307 aac cgc gga ttg ctg ccc cca gga ttc tcg ttg gta ggt tac ggc cgc Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu Val Gly Tyr Gly Arg

55

65

- 34

60

cgc gaa tgg tcc aaa gaa gac ttt gaa aaa tac gta cgc gat gcc gca 355 Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr Val Arg Asp Ala Ala 70 agt gct ggt gct cgt acg gaa ttc cgt gaa aat gtt tgg gag cgc ctc 403 Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn Val Trp Glu Arg Leu 90 gcc gag ggt atg gaa ttt gtt cgc ggc aac ttt gat gat gat gca gct 451 Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe Asp Asp Asp Ala Ala 105 110 ttc gac aac ctc gct gca aca ctc aag cgc atc gac aaa acc cgc ggc 499 Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile Asp Lys Thr Arg Gly 120 acc gcc ggc aac tgg gct tac tac ctg tcc att cca cca gat tcc ttc 547 Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile Pro Pro Asp Ser Phe 135 595 aca gcg gtc tgc cac cag ctg gag cgt tcc ggc atg gct gaa tcc acc Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly Met Ala Glu Ser Thr 150 155 gaa gaa gca tgg cgc cgc gtg atc atc gag aag cct ttc ggc cac aac 643 Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys Pro Phe Gly His Asn 170 691 ctc gaa tcc gca cac gag ctc aac cag ctg gtc aac gca gtc ttc cca Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val Asn Ala Val Phe Pro 185 gaa tot tot gtg tto oge ato gao cao tat ttg ggc aag gaa aca gtt 739 Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu Gly Lys Glu Thr Val 200 205 caa aac atc ctg gct ctg cgt ttt gct aac cag ctg ttt gag cca ctg 787 Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln Leu Phe Glu Pro Leu 215 220 tgg aac tcc aac tac gtt gac cac gtc cag atc acc atg gct gaa gat 835 Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile Thr Met Ala Glu Asp 230 235 att ggc ttg ggt gga cgt gct ggt tac tac gac ggc atc ggc gca gcc 883 Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp Gly Ile Gly Ala Ala cgc gac gtc atc cag aac cac ctg atc cag ctc ttg gct ctg gtt gcc 931 Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu Leu Ala Leu Val Ala 270 atg gaa gaa cca att tct ttc gtg cca gcg cag ctg cag gca gaa aag 979 Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln Leu Gln Ala Glu Lys 285 atc aag gtg ctc tct gcg aca aag ccg tgc tac cca ttg gat aaa acc 1027 Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr Pro Leu Asp Lys Thr 295 300 305

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				tac Tyr 315									1075
				gaa Glu									1123
				acc Thr									1171
				cgc Arg									1219
				ttt Phe									1267
-	_		-	ctt Leu 395			-			-		_	1315
	_	_		 ctc Leu		_							1363
				gac Asp									1411
			_	cct Pro	_	_		-		_	_		1459
_		_	-	agc Ser					 _		_	_	1507
				gat Asp 475									1555
				cca Pro									1603
				aac Asn						taat	ttaq	ggg	1652
gcaa	aaaa	atg a	atc										1665

<210> 244

<211> 514

<212> PRT

<213> Corynebacterium glutamicum

<400> 244

Val Ser Thr Asn Thr Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Pro Gln Asp Lys Arg Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val 20 25 30

Ile Phe Gly Val Thr Gly Asp Leu Ala Arg Lys Leu Leu Pro Ala 35 40 45

Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu 50 55 60

Val Gly Tyr Gly Arg Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr 65 70 75 80

Val Arg Asp Ala Ala Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn 85 90 95

Val Trp Glu Arg Leu Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe 100 105 110

Asp Asp Ala Ala Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile 115 120 125

Asp Lys Thr Arg Gly Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile 130 135 140

Pro Pro Asp Ser Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly 145 150 155 160

Met Ala Glu Ser Thr Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys 165 170 175

Pro Phe Gly His Asn Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val 180 185 190

Asn Ala Val Phe Pro Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu 195 200 205

Gly Lys Glu Thr Val Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln 210 215 220

Leu Phe Glu Pro Leu Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile 225 230 235 240

Thr Met Ala Glu Asp Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp 245 250 255

Gly Ile Gly Ala Ala Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu 260 265 270

Leu Ala Leu Val Ala Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln 275 280 285

Leu Gln Ala Glu Lys Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr 290 295 300

Pro Leu Asp Lys Thr Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln 305 310 315 320

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Gly Ser Glu Leu Val Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro Glu Ser Thr Thr Glu Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser Arg Arg Trp Ala Gly Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu Gly Arg Arg Val Thr Glu Ile Ala Val Val Phe Lys Asp Ala Pro His 370 375 380 Gln Pro Phe Asp Gly Asp Met Thr Val Ser Leu Gly Gln Asn Ala Ile 390 Val Ile Arq Val Gln Pro Asp Glu Gly Val Leu Ile Arq Phe Gly Ser Lys Val Pro Gly Ser Ala Met Glu Val Arg Asp Val Asn Met Asp Phe Ser Tyr Ser Glu Ser Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg Leu Ile Leu Asp Ala Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn 455 Glu Glu Val Glu Leu Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala 475 Trp Asp Ala Asp Gly Glu Pro Glu Asp Tyr Pro Ala Gly Thr Trp Gly Pro Lys Ser Ala Asp Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg 505 Arg Pro <210> 245 <211> 1203 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1180) <223> RXA02738 <400> 245 ttgttgttaa tcggtacaaa gggtcttaag cacatccctt acttgcctgc tctccttgag 60

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gat ctt gca cag ctc ggc act tcc act tgg ctc gac gac ctc tcc cgc 163 Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu Asp Asp Leu Ser Arg 15 10 20

gag Glu	cgc Arg.	att Ile	act Thr 25	tcc Ser	ggc Gly	aat Asn	ctc Leu	agc Ser 30	cag Gln	gtt Val	att Ile	gag Glu	gaa Glu 35	aag Lys	tct Ser	211
gta Val	gtc Val	ggt Gly 40	gtc Val	acc Thr	acc Thr	aac Asn	cca Pro 45	gct Ala	att Ile	ttc Phe	gca Ala	gca Ala 50	gca Ala	atg Met	tcc Ser	259
aag Lys	ggc Gly 55	gat Asp	tcc Ser	tac Tyr	gac Asp	gct Ala 60	cag Gln	atc Ile	gca Ala	gag Glu	ctc Leu 65	aag Lys	gcc Ala	gct Ala	ggc Gly	307
				cag Gln												355
				ctg Leu 90												403
gac Asp	ggc Gly	cgc Arg	gtg Val 105	tcc Ser	atc Ile	gag Glu	gtt Val	gac Asp 110	cca Pro	cgt Arg	atc Ile	tct Ser	gct Ala 115	gac Asp	cgc Arg	451
				gct Ala												499
				atc Ile												547
atc Ile 150	acc Thr	gac Asp	gct Ala	ttg Leu	gct Ala 155	gag Glu	ggc Gly	atc Ile	agc Ser	gtt Val 160	aac Asn	gtc Val	acc Thr	ttg Leu	atc Ile 165	595
				cgc Arg 170												643
				gct Ala												691
				ttc Phe												739
				gga Gly												787
				gct Ala												835
				ctg Leu 250												883
gca	tcc	acc	ggc	gtg	aag	aac	cct	gcg	tac	gct	gca	act	ctt	tac	gtt	931

Ala Ser Thr	Gly Val 265	Lys	Asn E		Ala Ty 270	yr Ala	Ala	Thr	Leu 275	Tyr	Val	
tcc gag ctg Ser Glu Leu 280			Asn 1									979
atc gac gcg Ile Asp Ala 295		Glu										1027
aac tcc gcg Asn Ser Ala 310												1075
ggc gtt gac Gly Val Asp		Asp	-		31n Va	_						1123
gac aag ttc Asp Lys Phe				Ser G	-	-			_	_	-	1171
cgc ctg aag Arg Leu Lys 360	tagaatc	agc a	cgcto	gcato	c agt							1203
<210> 246 <211> 360												
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<212> PRT <213> Coryn <400> 246 Met Ser His 1 Asp Asp Leu	Ile Asp 5 Ser Arg 20 Lys Ser	Asp Glu .	Leu A	Ala G Ile T Gly V 40	Thr Se 25 Val Th	er Gly	Asn Asn	Leu Pro 45	Ser 30 Ala	15 Gln Ile	Val Phe	
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<212> PRT <213> Coryn <400> 246 Met Ser His 1 Asp Asp Leu Ile Glu Glu 35 Ala Ala Ala 50 Leu Lys Ala	Ile Asp 5 Ser Arg 20 Lys Ser Met Ser Ala Gly	Asp Glu Val Lys Ala 70 Asn	Leu Arg 1 Val C Gly A 55	Ala G Ile T Gly V 40 Asp S	Thr Sec 25 Val The Sec Ty Asp Gl	er Gly Thr Yr Asp In Ala 75	Asn Ala 60 Val	Leu Pro 45 Gln Tyr	Ser 30 Ala Ile Ala	15 Gln Ile Ala Met	Val Phe Glu Ser 80	
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Gly Ser Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val 155 150 Asn Val Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala 165 170 Ala Phe Ile Glu Gly Ile Lys Gln Ala Ala Asn Gly His Asp Val 185 Ser Lys Ile His Ser Val Ala Ser Phe Phe Val Ser Arg Val Asp Val 200 Glu Ile Asp Lys Arg Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala 215 Leu Arg Gly Lys Ala Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val 230 235 Tyr Lys Glu Leu Phe Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr 245 Gln Arg Pro Leu Trp Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala 265 Ala Thr Leu Tyr Val Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr Met Pro Glu Gly Thr Ile Asp Ala Val Leu Glu Gln Gly Asn Leu His 295 Gly Asp Thr Leu Ser Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser 315 310 Gln Leu Glu Ala Leu Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu 330 325 Glu Thr Glu Gly Val Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu 340 Glu Ser Met Glu Ala Arg Leu Lys 355 <210> 247 <211> 2223 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(2200) <223> RXA02739 <400> 247 cctttgccaa atttgaacca attaacctaa gtcgtagatc tgatcatcgg atctaacgaa 60 aacgaaccaa aactttggtc ccggtttaac ccaggaagga ttg acc acc ttg acg Leu Thr Thr Leu Thr

ctg tca cct gaa ctt cag gcg ctc act gta cgc aat tac ccc tct gat

Leu	Ser	Pro	Glu	Leu 10	Gln	Ala	Leu	Thr	Val 15	Arg	Asn	Tyr	Pro	Ser 20	Asp	
						aag Lys										211
						tgt Cys										259
						tac Tyr 60										307
		_	-			tgg Trp				_						355
						acc Thr										403
				_	-	gac Asp	_	-	-	_	_			_		451
_						gag Glu										499
						cag Gln 140			-							547
_	-	_	_	_		cgt Arg										595
	_				_	cac His				-		_		_		643
						acc Thr										691
						atc Ile										739
						atc Ile 220										787
						cag Gln										835
						gca Ala										883

	250	255	5	260
_	e Ile Arg Val	-	e atc ggc ttc cca e Ile Gly Phe Pro 275	
			gct gct ctt ggc Ala Ala Leu Gly 290	
, , , ,	-		a ttc gat cct gag / Phe Asp Pro Glu 305	-
			c acc cgc tcc ctc s Thr Arg Ser Leu 320	
			g gtc aag ttc gat n Val Lys Phe Asp	
	n Pro Glu Asn		g ttc gat cgc ctg n Phe Asp Arg Leu 355	
			g ctc cca aca tgg 1 Leu Pro Thr Trp 370	-
			tcc gag gct gca Ser Glu Ala Ala 385	
, , , ,	-		g ggc ggt tcc gct o Gly Gly Ser Ala 400	-
			c tee eet tee tte 7 Ser Pro Ser Phe 5	
	r Thr Glu Thr		gag cct tac ggc Glu Pro Tyr Gly 435	
			g gga tcc atc ctc : Gly Ser Ile Leu 450	
		-	c ggc gga acc ttc c Gly Gly Thr Phe 465	
			c ctt gca gct ctc g Leu Ala Ala Leu 480	
			c tcc atc ggt ctg o Ser Ile Gly Leu o	

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	ggc Gly														1651
	cca Pro		_		-	_	_		_	_				_	1699
	gct Ala 535														1747
_	ctg Leu		_	_		_		_	_	_			_	 _	1795
	gct Ala														1843
	gaa Glu														1891
	gca Ala														1939
	gtt Val 615														1987
	tac Tyr														2035
_	gaa Glu	-													2083
	cgt Arg														2131
	ctg Leu													gcg Ala	2179
_	aag Lys 695	_					taat	ttgc	ect o	gctgi	tttt	ca go	et		2223

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<211> 700

<212> PRT

<213> Corynebacterium glutamicum

<400> 248

Leu Thr Thr Leu Thr Leu Ser Pro Glu Leu Gln Ala Leu Thr Val Arg

10 1 5 15 Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala Val Asp Thr Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly Ser Gly His Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr Leu Tyr Gln Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala Gly Arg Asp Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln Tyr Ile Gln Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu Lys Ala Leu 105 Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr Arg His Thr 120 Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly Leu Ala Ser 135 Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly Leu Phe Asp 150 155 Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His Ile Tyr Val 170 Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser Glu Ala Ser 185 Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val Phe Trp Asp 200 Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala Phe Asn Glu 215 Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr Ile Glu Val Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val Ala Glu Ala Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg Thr Ile Ile 265 Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val His Gly Ala 275 Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu Leu Gly Phe 295 Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile Ala His Thr Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala Trp Gln Val 330

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Lys Phe Asp Glu Trp Ala Ala Ala Asn Pro Glu Asn Lys Ala Leu Phe 345 Asp Arg Leu Asn Ser Arg Glu Leu Pro Ala Gly Tyr Ala Asp Glu Leu 360 Pro Thr Trp Asp Ala Asp Glu Lys Gly Val Ala Thr Arg Lys Ala Ser Glu Ala Ala Leu Gln Ala Leu Gly Lys Thr Leu Pro Glu Leu Trp Gly Gly Ser Ala Asp Leu Ala Gly Ser Asn Asn Thr Val Ile Lys Gly Ser 405 410 Pro Ser Phe Gly Pro Glu Ser Ile Ser Thr Glu Thr Trp Ser Ala Glu 425 Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His Ala Met Gly 440 Ser Ile Leu Asn Gly Ile Ser Leu His Gly Gly Thr Arg Pro Tyr Gly 455 Gly Thr Phe Leu Ile Phe Ser Asp Tyr Met Arg Pro Ala Val Arg Leu 470 475 Ala Ala Leu Met Glu Thr Asp Ala Tyr Tyr Val Trp Thr His Asp Ser 485 Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Thr Leu 505 Ala Ala Leu Arg Ala Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp 520 Ala Asn Glu Thr Ala Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu 535 Gly Pro Lys Gly Leu Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu Gly Thr Lys Glu Lys Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val 570 Leu Val Glu Gly Ser Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser Gly Ser Glu Val Gln Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala 600 Glu Gly Val Ala Ala Arg Val Val Ser Val Pro Cys Met Asp Trp Phe 610 615 Gln Glu Gln Asp Ala Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val 635 Thr Ala Arg Val Ser Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg

Phe Leu Gly Thr Gln Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala 665 Ser Ala Asp Tyr Gln Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp 675 Ala Val Val Ala Ala Ala Lys Asp Ser Ile Asn Gly 695 <210> 249 <211> 793 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (48)..(770) <223> RXA00965 <400> 249 agattgcggg cctcggcttc attgaaaaca agacggtgtt tgaataaatg aca act 56 Met Thr Thr ttc cac gat ctt ccg ctg gag gag cgg ctg aca ctg gcc agg ttg ggc 104 Phe His Asp Leu Pro Leu Glu Glu Arg Leu Thr Leu Ala Arg Leu Gly 10 aca too cao tao too ogt cag oto too oto gtg gao aac got gag tto 152 Thr Ser His Tyr Ser Arg Gln Leu Ser Leu Val Asp Asn Ala Glu Phe 20 25 30 ggc gag cat tcc ctg cta gaa ggg tgg act cgt tcc cac ctc att gcc 200 Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His Leu Ile Ala 40 cac gtg gca tac aac gcc atc gca ctg tgc aac ctc atg cac tgg gca 248 His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met His Trp Ala 55 296 aat act ggt gag gaa acc cca atg tac gtg tcg cca gaa gcg cgc aac Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu Ala Arg Asn 70 75 gag gaa att gcc tac ggt tcc acg ctc aat ccc gat gcg ttg cgt aac 344 Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala Leu Arg Asn 85 90 ctg cat gaa cac tcc gtc gca cgc ctg gac gtg gct tgg cgt gaa acg Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp Arg Glu Thr 100 105 110 115 440 tct gaa gat gct tgg tca cac gag gtt ctg aca gct cag gga cgc act Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln Gly Arg Thr 120 130 488 gtc cca gct agt gaa aca ttg tgg atg cgt tcc cgc gaa gtc tgg atc

Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu Val Trp Ile

135

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cac gca gtt His Ala Val 150												
gtc atc ctg Val Ile Leu 165	_		-	-	_				_			_
caa gga gcc Gln Gly Ala 180												
cgc tac ccc Arg Tyr Pro		a Pro										
ctt gca ggc Leu Ala Gly												
act tct tcc Thr Ser Ser 230			-				_	_		_		
tagtttccac	acattct	aa at	g									
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<400> 250							~ 3		_	_,	_	- 1
_		s Asp				Glu 10	Glu	Arg	Leu	Thr	Leu 15	Ala
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<400> 250 Met Thr Thr 1 Arg Leu Gly Ala Glu Phe 35 Leu Ile Ala	Phe His	S Asp	Leu Tyr Ser Tyr 55	Pro Ser Leu 40 Asn	Leu Arg 25 Leu Ala	10 Gln Glu Ile	Leu Gly Ala	Ser Trp Leu 60	Leu Thr 45 Cys	Val 30 Arg Asn	15 Asp Ser Leu	Asn His Met
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<pre><400> 250 Met Thr Thr 1 Arg Leu Gly Ala Glu Phe</pre>	Phe His	Asp His His Ala Gly 70 Ile Glu Asp	Leu Tyr Ser Tyr 55 Glu Ala His	Pro Ser Leu 40 Asn Glu Tyr Ser Trp 120	Leu Arg 25 Leu Ala Thr Gly Val 105 Ser	10 Gln Glu Ile Pro Ser 90 Ala His	Leu Gly Ala Met 75 Thr Arg	Ser Trp Leu 60 Tyr Leu Leu Val	Leu Thr 45 Cys Val Asn Asp	Val 30 Arg Asn Ser Pro Val 110	15 Asp Ser Leu Pro Asp 95 Ala Ala	Asn His Met Glu 80 Ala Trp Gln

145	150	155 160
Ile Pro Glu Val Ile 169	-	Ala Glu Ile Thr Gln Lys 175
Trp Thr Ser Gln Gly 180	Ala Gly Glu Gly Leu 185	Val Leu Leu Asp Glu Pro 190
Ser Ser Thr Arg Tyn 195	Pro Ala Ala Pro Gly 200	Gln Asp Glu Val Val 205
Ser Gly Ser Leu Ala 210	Gly Ile Val Arg Tyr 215	Ala Ala Gly Arg Gly Ser 220
Asp Gly Val Thr Ser 225	Ser Thr Gly Glu Val 230	Pro Glu Pro Pro Arg Trp 235 240
Leu		
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ttgctgacac cgggctai	gc cgtcaagtac gatcaa ggc gtt gta ggc cta Gly Val Val Gly Leu	taac atg act aat gga gat Met Thr Asn Gly Asp 1 5 gca gta atg ggc tca aac Ala Val Met Gly Ser Asn
cctcctgtga cctggtaa ttgctgacac cgggctaa aat ctc gca cag atc Asn Leu Ala Gln Ile ctc gcc cgc aac ttc	gc cgtcaagtac gatcaa ggc gtt gta ggc cta Gly Val Val Gly Leu 15	taac atg act aat gga gat Met Thr Asn Gly Asp 1 5 gca gta atg ggc tca aac Ala Val Met Gly Ser Asn
cctcctgtga cctggtaa ttgctgacac cgggctaa aat ctc gca cag atc Asn Leu Ala Gln Ile ctc gcc cgc aac ttc Leu Ala Arg Asn Phe 25 cgc agc act gac aac	egc cgtcaagtac gatcaa eggc gtt gta ggc cta e Gly Val Val Gly Leu 15 egcc cgc aac ggc aac e Ala Arg Asn Gly Asn 30	taac atg act aat gga gat Met Thr Asn Gly Asp 1
aat ctc gca cag atc Asn Leu Ala Gln Ile ctc gcc cgc aac ttc Leu Ala Arg Asn Phe 25 cgc agc act gac aaa Arg Ser Thr Asp Lys 40 ggc aac ttc atc ccc	e ggc gtt gta ggc cta e Gly Val Val Gly Leu 15 e gcc cgc aac ggc aac e Ala Arg Asn Gly Asn 30 a acc gac aag ctc atc e Thr Asp Lys Leu Ile 45 e tct gca acc gtc gaa	taac atg act aat gga gat Met Thr Asn Gly Asp 1 5 gca gta atg ggc tca aac 163 Ala Val Met Gly Ser Asn 20 act gtc gct gtc tac aac 211 Thr Val Ala Val Tyr Asn 35 gcc gat cac ggc tcc gaa 259 Ala Asp His Gly Ser Glu
aat ctc gca cag atc Asn Leu Ala Gln Ile ctc gcc cgc aac ttc Leu Ala Arg Asn Phe 25 cgc agc act gac aac Arg Ser Thr Asp Lys 40 ggc aac ttc atc ccc Gly Asn Phe Ile Pro 55	ggc cgtcaagtac gatcaa ggc gtt gta ggc cta gGly Val Val Gly Leu 15 gcc cgc aac ggc aac Ala Arg Asn Gly Asn 30 acc gac aag ctc atc Thr Asp Lys Leu Ile 45 tct gca acc gtc gaa Ser Ala Thr Val Glu 60 gcc atc atc atg gtt	taac atg act aat gga gat Met Thr Asn Gly Asp 5 gca gta atg ggc tca aac 163 Ala Val Met Gly Ser Asn 20 act gtc gct gtc tac aac 211 Thr Val Ala Val Tyr Asn 35 gcc gat cac ggc tcc gaa 259 Ala Asp His Gly Ser Glu 50 gag ttc gta gca tcc ctg 307 Glu Phe Val Ala Ser Leu

					gcc Ala									451
					ggt Gly									499
		_	_	 _	ctc Leu 140					_				547
					tcc Ser									595
					cca Pro									643
					atg Met									691
_	_	-		 	gca Ala				_		-	_		739
					gct Ala 220									787
	_	_			atc Ile	-		_	_	-			_	835
	_	_	_		aag Lys			-	_		_	_	_	883
					gga Gly									931
					ggc Gly									979
					cag Gln 300									1027
					ctg Leu									1075
					cgt Arg									1123

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														aac Asn		1171
	-	_	_		_	_		_				_		ggc Gly	_	1219
		_	_	_				-		_		-		gat Asp	_	1267
														agc Ser		1315
														gcc Ala 420		1363
														tac Tyr		1411
														gga Gly		1459
_	_								_	_		_	_	gat Asp		1507
					tgg Trp 475			_	_			_	_	-		1552
taaa	aggct	ct o	ccttt	taad	ca ca	aa										1575
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)> 25 Thr		Gly	Asp 5	Asn	Leu	Ala	Gln	Ile 10	Gly	Val	Val	Gly	Leu 15	Ala	
Val	Met	Gly	Ser	Asn	Leu	Ala	Arg	Asn	Phe	Ala	Arg	Asn	Gly	Asn	Thr	

Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala 40

Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu

Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln

Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met

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85 90 95 Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp 105 Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val 115 120 Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser 135 Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys 215 Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala 235 Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala 280 Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly 345 Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile 355 360 Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val 375 380 Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro 385 390 395 Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val 405 410

Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser 420 425 Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg 455 Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser 475 Glu Val Glu Ala <210> 253 <211> 1537 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1537) <223> FRXA00999 <400> 253 cctcctgtga cctggtaaaa tcgccactac ccccaaatgg tcacaccttt taggccgatt 60 ttgctgacac cgggctatgc cgtcaagtac gatcaataac atg act aat gga gat Met Thr Asn Gly Asp aat ctc gca cag atc ggc gtt gta ggc cta gca gta atg ggc tca aac 163 Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Ser Asn ctc gcc cgc aac ttc gcc cgc aac ggc aac act gtc gct gtc tac aac 211 Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr Val Ala Val Tyr Asn cgc agc act gac aaa acc gac aag ctc atc gcc gat cac ggc tcc gaa 259 Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala Asp His Gly Ser Glu 45 ggc aac ttc atc cct tct gca acc gtc gaa gag ttc gta gca tcc ctg 307 Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu Phe Val Ala Ser Leu 60 gaa aag cca cgc cgc gcc atc atc atg gtt cag gct ggt aac gcc acc 355 Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln Ala Gly Asn Ala Thr 75 gac gca gtc atc aac cag ctg gca gat gcc atg gac gaa ggc gac atc 403 Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met Asp Glu Gly Asp Ile 90 95 ate ate gae gge gge aac gee etc tac ace gae ace att egt ege gag 451

Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp Thr Ile Arg Arg Glu

110

										gtc Val						499
										tcc Ser						547
										ctg Leu 160						595
_		_	_				-	_		cac His				-		643
										ggc Gly						691
										ctc Leu						739
										aag Lys						787
_	_	_					_			gca Ala 240		-			_	835
	_	_	_			_				gac Asp	_		_	_	-	883
										gtc Val						931
										gct Ala						979
			-		_	-	-	-	-	gca Ala	_					1027
										ggc Gly 320						1075
										gca Ala						1123
tac Tyr	gca Ala	cag Gln	ggc Gly 345	ttc Phe	gac Asp	gag Glu	atc Ile	aag Lys 350	gct Ala	ggc Gly	tcc Ser	gac Asp	gag Glu 355	aac Asn	aac Asn	1171

Trp Asp Val A	jac cct c Asp Pro A										1219
atc att cgc g Ile Ile Arg A 375											1267
aac gct gaa c Asn Ala Glu I 390	eu Glu S	-	_	_				_	_		1315
ctc ggc gac c Leu Gly Asp I	_			_			_		-		1363
cag ctt ggc c Gln Leu Gly I 4	-			e Āla			_				1411
gac agc ctg c Asp Ser Leu A 440			_	_	-	_				-	1459
cgc gac ttc t Arg Asp Phe F 455		_		_	-		_	_	_		1507
tcc ttc cac a Ser Phe His T											1537
470		75	01,	ping							
	4	75	_	P 1119							
470 <210> 254 <211> 479 <212> PRT	4 pacterium	75 glutam	nicum		Gly	Val	Val	Gly	Leu 15	Ala	
<pre>470 <210> 254 <211> 479 <212> PRT <213> Coryneb <400> 254 Met Thr Asn G</pre>	acterium Gly Asp A 5	75 glutam sn Leu	nicum Ala Gl	n Ile 10 n Phe				_	15		
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Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val

120 115 125 Gly Ala Gly Ile Ser Gly Gly Glu Gly Ala Leu Asn Gly Pro Ser 135 Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu 145 Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His 170 Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys 215 Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala 235 Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala 280 Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly 315 Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val 375 Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro 385 390 395 Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val 405 410 Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser 420 425 Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala 440

135

Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg 450 455 Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg 470 475 <210> 255 <211> 1326 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1303) <223> RXN02596 <400> 255 aaggtatetg ggtgtggata tgeeetgeta aetggagaaa ettggeeega tegggtgtet 60 gaaatttcgg caacgccgaa tgtaagttag tgtcgaatgc atg acg gaa tcg aaa 115 Met Thr Glu Ser Lys aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg 163 Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val 10 15 211 gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu cgc cgc tcg cac ctc ggt ggc aat gct tac tct gaa gca gaa cca gag 259 Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu 40 45 307 acc ggc att gaa atc cac aaa tac ggc gcg cac ctc ttc cac acc tcc Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser 60 aac aca cgc gtg tgg gaa tac gtc aac cag ttc acc agt ttc acc ggc 355 Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly 70 75 tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc 403 Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe 90 ccc atg gga ctg ggc ctg att aac cag ttc ttc ggc aag tac tac agc 451 Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser 105 110 cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat 499 Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp 120 125 tee tee gae gee ace aac ete gaa gaa aag gee att tee ete att ggt 547 Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly

140

_	cca Pro				_			_	_			_	_	_		595
_	act Thr	-		_				-					_	_		643
_	cgc Arg						_				-			_		691
	ccc Pro		_				_		_	_	_	_	_			739
	ctt Leu 215		_	-	_		_		-			_	-	_	_	787
_	ctc Leu	_	_	_			_	_			_					835
	gac Asp						-			_	_			_		883
	gac Asp															931
	gtg Val															979
	ttc Phe 295	_						_	_	_	_			-	-	1027
	acc Thr															1075
	cct Pro															1123
	tac Tyr															1171
	ggc Gly		_	_		_		_			_	_		_	_	1219
	ggt Gly 375															1267
gaa	gaa	ggc	aca	ccg	cta	gag	cag	gaa	cgc	gga	cac	taaa	aagga	aag		1313

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ggcatctccc aca 1326

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<211> 401

<212> PRT

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<400> 256

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Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser 35 40 45

Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His 50 55 60

Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe 65 70 75 80

Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly 85 90 95

Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe 100 105 110

Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln
115 120 125

Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala 130 $$135\$

Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr 145 150 155 160

Thr Ala Lys Gln Trp Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn 165 170 175

Ile Thr Arg Leu Pro Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn 180 185 190

Asp Thr Tyr Glu Gly Leu Pro Thr Asp Gly Tyr Ala Ala Trp Leu Glu 195 200 205

Lys Met Ala Glu His Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp 210 215 220

Phe Asp Val Arg Asp Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val 225 230 235 240

Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys 245 250 255

Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly

260 265 270 Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro 280 Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg Asp Asp 290 295 Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe 310 315 Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu 360 Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys 375 Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu Arg Gly 395 His <210> 257 <211> 512 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(489) <223> FRXA02596 <400> 257 cct qtq qtc tac acc qqc cca ctc qac ctc tac ttc aac tac gca qaq 48 Pro Val Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu qqc aaq ctq qqa tqq cqc acc ctc qac ttt qaa acc qaa gta gta gaa Gly Lys Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu 20 acc ggt gac ttc caa gga acc cca gtg atg aac tac aac gat gcg gac 144 Thr Gly Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp 35 40 gta cct ttc acc cgc atc cac gag ttc cgt cac ttc cac cca gag cgt 192 Val Pro Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg 50 55 60 gat gac agt tac ccc aag gat aag acc gtc atc atg cgc gag ttc tcc 240 Asp Asp Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser 65 70 75

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Arg Phe Ala Asp			t tat tac cc o Tyr Tyr Pr 90		
gac gac cga gac Asp Asp Arg Asp 100	Met Leu		r Arg Leu Le		
gct gct aat aat Ala Ala Asn Asr 115					
tac ctc gac atc Tyr Leu Asp Met 130				u Ser Met	
aac aag ctg gtg Asn Lys Leu Val 145	-	-			
cgc gga cac taa Arg Gly His	aaggaag g	gcatctccc	aca		
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Gly Lys Leu Gly 20		Thr Leu Asy	•	r Glu Val 30	Val Glu
Thr Gly Asp Phe	a1 a1				
35	Gin Gly	Thr Pro Val	l Met Asn Ty	r Asn Asp 45	Ala Asp
35 Val Pro Phe Thr 50		40	e Arg His Ph	45	
Val Pro Phe Thr	Arg Ile	40 His Glu Pho	e Arg His Ph 6	45 e His Pro O	Glu Arg
Val Pro Phe Thr 50 Asp Asp Ser Tyr	Arg Ile Pro Lys 70	40 His Glu Pho 55 Asp Lys Th	e Arg His Ph 6 r Val Ile Me 75	45 e His Pro 0 t Arg Glu	Glu Arg Phe Ser
Val Pro Phe Thr 50 Asp Asp Ser Tyr 65	Arg Ile Pro Lys 70 Asn Glu 85	40 His Glu Pho 55 Asp Lys Th	e Arg His Ph 6 r Val Ile Me 75 o Tyr Tyr Pr 90 r Arg Leu Le	45 e His Pro 0 t Arg Glu o Ile Asn	Glu Arg Phe Ser 80 Thr Pro 95
Val Pro Phe Throson Son Son Son Son Son Son Son Son Son S	Arg Ile Pro Lys 70 Asn Glu 85 Met Leu	40 His Glu Pho 55 Asp Lys Th: Asp Glu Pro Lys Gln Ty: 10:	e Arg His Ph 6 r Val Ile Me 75 o Tyr Tyr Pr 90 r Arg Leu Le	45 e His Pro 0 t Arg Glu o Ile Asn u Ala Ala 110	Glu Arg Phe Ser 80 Thr Pro 95 Glu Glu
Val Pro Phe Throson Son Son Son Son Son Son Son Son Son S	Arg Ile Pro Lys 70 Asn Glu 85 Met Leu Lys Val His Met	40 His Glu Pho 55 Asp Lys The Asp Glu Pro Lys Gln Tye 10 Leu Phe Gle 120	e Arg His Ph 6 r Val Ile Me 75 r Tyr Tyr Pr 90 r Arg Leu Le 5	e His Pro t Arg Glu o Ile Asn u Ala Ala 110 u Gly Thr 125 u Ser Met	Glu Arg Phe Ser 80 Thr Pro 95 Glu Glu Tyr Gln

Arg Gly His

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598 cag Gln <210> 260 <211> 166 <212> PRT <213> Corynebacterium glutamicum <400> 260 Met Thr Glu Ser Lys Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln 120 Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala 135 Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr 155 Thr Ala Lys Gln Trp Gln <210> 261 <211> 668 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(645) <223> RXA02572 <400> 261 gcg gtc gct gag att tgc gag ccg acc ggc gcc gat gcg gtt gcg ctt 48 Ala Val Ala Glu Ile Cys Glu Pro Thr Gly Ala Asp Ala Val Ala Leu 10

gtg gat gcc atc ggt cac gac gat cgt atc ggc cga aag ttc tta ggc

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Val	Asp	Ala	Ile 20	Gly	His	Asp	Asp	Arg 25	Ile	Gly	Arg	Lys	Phe 30	Leu	Gly	
		_			ggt Gly			_	_			-		_	_	144
					ggc Gly											192
_	-		-	-	tcc Ser 70			_	-			-	_			240
					atg Met											288
					gca Ala											336
	_		_	_	gtc Val			_		_		_				384
					ccg Pro											432
_	_		_		gcg Ala 150		_							_	_	480
			-		gcc Ala		_			_		-	_		_	528
	_				Gly	_	_		_	_	_			_		576
					gtt Val											624
-				_	aac Asn		tagt	gegg	gtg g	gatca	aggc	ia ad	ic			668

<210> 262

<211> 215

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

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Val Asp Ala Ile Gly His Asp Asp Arg Ile Gly Arg Lys Phe Leu Gly 20 25 30

Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala 35 40 45

Phe Met Ala Arg Ala Gly Glu Leu Gly Ala Asp Gln Ala Leu Thr Phe 50 55 60

Leu Arg Glu Val Asp Ser Ile Asn Met Arg Arg Arg Asp Arg Val Val 65 70 75 80

Gln Leu Ala Lys Glu Met Cys Gly Gly Ser Leu Leu Gly Lys Arg Val 85 90 95

Thr Val Leu Gly Ala Ala Phe Lys Pro Asn Ser Asp Asp Val Arg Asp 100 105 110

Ser Pro Ala Leu Ser Val Ala Gly Ser Leu Ser Leu Gln Gly Ala Ala 115 120 125

Val Ser Val Tyr Asp Pro Glu Ala Met Asp Asn Ala Arg Arg Val Phe 130 135 140

Pro Thr Leu Ser Tyr Ala Ser Ser Thr Lys Glu Ala Leu Ile Asp Ala 145 150 155 160

His Leu Val Val Leu Ala Thr Glu Trp Gln Glu Phe Arg Asp Leu Asp 165 170 175

Pro Glu Val Ala Gly Gly Val Val Glu Lys Arg Ala Ile Ile Asp Gly 180 185 190

Arg Asn Val Leu Asp Val Ala Lys Trp Lys Ala Ala Gly Trp Glu Met 195 200 205

Glu Ala Leu Gly Arg Asn Leu 210 215

<210> 263

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1201)

<223> RXA02485

<400> 263

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tacgcgttgc catgaggata agactaccgt tagtggggtg ttg gat tca tcg cta 115

Leu Asp Ser Ser Leu

1 5

gcc cag gaa atc gcc gcg atc gac ggc gtc gaa ctc gat tcg gaa gtc 163 Ala Gln Glu Ile Ala Ala Ile Asp Gly Val Glu Leu Asp Ser Glu Val 10 15 20

												aaa Lys				211
												gcc Ala 50				259
	_	_	_							-		ggc Gly				307
	-		_	-		-	_	-	_		-	gtc Val			_	355
												ctc Leu				403
												gtg Val				451
												tcc Ser 130				499
		_					_			_	_	gtt Val		_	_	547
		_	_	_			_	_				caa Gln	_			595
_	-	_		-		_				_		tcc Ser				643
			_	-	_	_	_			_		cag Gln				691
_		_			_		_			_	_	gga Gly 210	_	_		739
												gtc Val				787
_	-	-	-		_		_	-	-			atg Met	_		-	835
												ttc Phe				883
atc	gtc	gac	сса	gcc	ctt	gcc	gac	gca	gtc	ttt	gaa	aaa	gtc	ggc	gaa	931



Ile	Val	Asp	Pro 265	Ala	Leu	Ala	Asp	Ala 270	Val	Phe	Glu	Lys	Val 275	Gly	Glu	
		_		_			gcc Ala 285		_			_				979
_	-				_	_	gcc Ala				_					1027
_		-		_		_	agc Ser						-			1075
							tcc Ser									1123
							acc Thr						-		_	1171
	Val					_	atc Ile 365	_		tgaa	attt	icc (gacgi	ccct	ig .	1221
gca																1224
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130 135 140 Glu Val Ser Asp Val Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr 150 155 His Gln Val Ser Trp Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg 165 170 Tyr Ser Asn Leu Lys Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu 180 185 Leu Gln Leu Leu Thr Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu 195 Leu Gly Arg Arg Leu Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg 215 Pro Val Arg Met Val Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys 225 230 235 Gly Met Val Val Glu His Thr Asp His Asp Thr Trp Ser Ala Gly Ser 250 Phe Phe Thr Asn Pro Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe 265 Glu Lys Val Gly Glu Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly 280 Lys Glu Lys Leu Ser Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys 295 Lys Gly His Pro Gly Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His 315 Thr Leu Ala Leu Thr Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val 325 Ala Leu Ala Lys Glu Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val 345 Thr Leu Val Pro Glu Pro Val Trp Ile Gly Ile Ser Ile Asp Asp 360 <210> 265 <211> 1124 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(1101) <223> RXA01216 <400> 265 acc gac cac act ctg tct gca ctg ctg gat gca cac gtg gaa gtt cca Thr Asp His Thr Leu Ser Ala Leu Leu Asp Ala His Val Glu Val Pro 10 acc gct gtc acc gtg ttg acc atg cgt ctg gat gac ccc acc ggc tac

48

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Thr	Ala	Val	Thr 20	Val	Leu	Thr	Met	Arg 25	Leu	Asp	Asp	Pro	Thr 30	Gly	Tyr	
	_			_		_	-		gaa Glu	_		_		_		144
									gcc Ala							192
	_		-		_	-	_		ttg Leu	_		_	_	_	_	240
_	_		_		_	_			ctg Leu 90		_		_	_	_	288
		-	_						gtg Val	_	_			-	_	336
									gat Asp							384
_		_	-			_	-		gtc Val		-	_	_	_		432
									acc Thr							480
Gly 145 tct	Ala	Thr gga	Ile	Val gac	Asp 150 gtg	Pro	Ala	Thr		Trp 155 ggc	Ile	Asp	Val	Glu aag	Val 160 ggc	480 528
Gly 145 tct Ser	Ala atc Ile act	Thr gga Gly gtc Val	Ile cgc Arg	yal gac Asp 165 gga Gly	Asp 150 gtg Val gac Asp	Pro atc Ile cgc	Ala atc Ile gtt Val	Thr cac His gaa Glu	CCt Pro 170 gtt Val	Trp 155 ggc Gly ggt	Ile acc Thr	Asp cag Gln gac Asp	Val ctc Leu	aag Lys 175 acc	Val 160 ggc Gly ttg	
Gly 145 tct Ser gaa Glu	Ala atc Ile act Thr	Thr gga Gly gtc Val	cgc Arg atc Ile 180	yal gac Asp 165 gga Gly	Asp 150 gtg Val gac Asp	Pro atc Ile cgc Arg	Ala atc Ile gtt Val	Thr cac His gaa Glu 185 gca	CCt Pro 170 gtt Val	Trp 155 ggc Gly ggt Gly	acc Thr cca Pro	Asp cag Gln gac Asp	ctc Leu acc Thr 190	aag Lys 175 acc Thr	Val 160 ggc Gly ttg Leu	528
Gly 145 tct Ser gaa Glu acc Thr	Ala atc Ile act Thr aac Asn	Thr gga Gly gtc Val atg Met 195 tcc	cgc Arg atc Ile 180 acc Thr	yal gac Asp 165 gga Gly atc Ile	Asp 150 gtg Val gac Asp ggc Gly	atc Ile cgc Arg gac Asp	Ala atc Ile gtt Val ggc Gly 200 aac	Thr cac His gaa Glu 185 gca Ala	Thr cct Pro 170 gtt Val tcc	Trp 155 ggc Gly ggt Gly gta Val	acc Thr cca Pro atc Ile	Asp cag Gln gac Asp cgc Arg 205	ctc Leu acc Thr 190 acc Thr	aag Lys 175 acc Thr	Val 160 ggc Gly ttg Leu ggt Gly	528 576
Gly 145 tct Ser gaa Glu acc Thr ttc Phe	Ala atc Ile act Thr aac Asn gac Asp 210 cgc	Thr gga Gly gtc Val atg Met 195 tcc Ser cca	cgc Arg atc Ile 180 acc Thr	yal gac Asp 165 gga Gly atc Ile atc	Asp 150 gtg Val gac Asp ggc Gly ggt Gly	Pro atc Ile cgc Arg gac Asp gaa Glu 215 ctg	Ala atc Ile gtt Val ggc Gly 200 aac Asn	Thr cac His gaa Glu 185 gca Ala gcc Ala cca	Thr cct Pro 170 gtt Val tcc Ser acc	Trp 155 ggc Gly ggt Gly gta Val gtt	acc Thr cca Pro atc Ile ggc Gly 220 aag	cag Gln gac Asp cgc Arg 205 ccc Pro	ctc Leu acc Thr 190 acc Thr	aag Lys 175 acc Thr cac His acc	Val 160 ggc Gly ttg Leu ggt Gly tac Tyr	528576624
Gly 145 tct Ser gaa Glu acc Thr ttc Phe atc Ile 225 gta	Ala atc Ile act Thr aac Asn gac Asp 210 cgc Arg	Thr gga Gly gtc Val atg Met 195 tcc Ser cca Pro	cgc Arg atc Ile 180 acc Thr acc Thr	gac Asp 165 gga Gly atc Ile acc Thr	Asp 150 gtg Val gac Asp ggc Gly ggt Gly aca Thr 230 gcc	etc Ile cgc Arg gac Asp gaa Glu 215 ctg Leu	Ala atc Ile gtt Val ggc Gly 200 aac Asn gga Gly atc	Thr cac His gaa Glu 185 gca Ala gcc Ala cca Pro	Thr cct Pro 170 gtt Val tcc Ser acc Thr	Trp 155 ggc Gly ggt Gly gta Val ggc Gly 235 ggc	acc Thr cca Pro atc Ile ggc Gly 220 aag Lys	cag Gln gac Asp cgc Arg 205 ccc Pro	ctc Leu acc Thr 190 acc Thr ttc Phe ggt Gly	aag Lys 175 acc Thr cac His acc Thr	Val 160 ggc Gly ttg Leu ggt Gly tac Tyr	528576624672

260 265 270 gcc tcc tct gtc ttc gtg aac tac gac ggt gaa aac aag cac cac acc 864 Ala Ser Ser Val Phe Val Asn Tyr Asp Gly Glu Asn Lys His His Thr 275 280 285 acc atc ggc agc cac gtt cgc act ggt tct gac acc atg ttt atc gct 912 Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp Thr Met Phe Ile Ala 290 295 cca gtg acc gtg ggt gac gga gcg tat tcc gga gcc ggt aca gta att 960 Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile 305 310 aaa gac gat gtt ccg cca gga gcc ctt gcc gtg tcc ggc gga cgc caa 1008 Lys Asp Asp Val Pro Pro Gly Ala Leu Ala Val Ser Gly Gly Arg Gln 325 cga aac atc gaa ggc tgg gtg caa aag aag cgc cct gga acc gct gca 1056 Arg Asn Ile Glu Gly Trp Val Gln Lys Lys Arg Pro Gly Thr Ala Ala 340 345 gca caa gcc gca gaa gcc gcc caa aac gtc cac aac cag gaa ggc 1101 Ala Gln Ala Ala Glu Ala Gln Asn Val His Asn Gln Glu Gly taagcaggat cctcatgact gct 1124 <210> 266 <211> 367 <212> PRT <213> Corynebacterium glutamicum <400> 266 Thr Asp His Thr Leu Ser Ala Leu Leu Asp Ala His Val Glu Val Pro Thr Ala Val Thr Val Leu Thr Met Arg Leu Asp Asp Pro Thr Gly Tyr Gly Arg Ile Val Arg Asn Glu Glu Gly Glu Val Thr Ala Ile Val Glu Gln Lys Asp Ala Ser Ala Glu Val Gln Ala Ile Asp Glu Val Asn Ser Gly Val Phe Ala Phe Asp Ala Ala Ile Leu Arg Ser Ala Leu Ala Glu Leu Lys Ser Asp Asn Ala Gln Gly Glu Leu Tyr Leu Thr Asp Val Leu 85 Gly Ile Ala Arg Gly Glu Gly His Pro Val Arg Ala His Thr Ala Ala 105 Asp Ala Arg Glu Leu Ala Gly Val Asn Asp Arg Val Gln Leu Ala Glu 115 120 Ala Gly Ala Glu Leu Asn Arg Arg Thr Val Ile Ala Ala Met Arg Gly 135

Gly Ala Thr Ile Val Asp Pro Ala Thr Thr Trp Ile Asp Val Glu Val 145 150 155 Ser Ile Gly Arg Asp Val Ile Ile His Pro Gly Thr Gln Leu Lys Gly 170 Glu Thr Val Ile Gly Asp Arg Val Glu Val Gly Pro Asp Thr Thr Leu 185 190 Thr Asn Met Thr Ile Gly Asp Gly Ala Ser Val Ile Arg Thr His Gly 200 Phe Asp Ser Thr Ile Gly Glu Asn Ala Thr Val Gly Pro Phe Thr Tyr Ile Arg Pro Gly Thr Thr Leu Gly Pro Glu Gly Lys Leu Gly Gly Phe Val Glu Thr Lys Lys Ala Thr Ile Gly Arg Gly Ser Lys Val Pro His 245 Leu Thr Tyr Val Gly Asp Ala Thr Ile Gly Glu Glu Ser Asn Ile Gly 265 Ala Ser Ser Val Phe Val Asn Tyr Asp Gly Glu Asn Lys His His Thr Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp Thr Met Phe Ile Ala 295 Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile 305 315 Lys Asp Asp Val Pro Pro Gly Ala Leu Ala Val Ser Gly Gly Arg Gln 325

Arg Asn Ile Glu Gly Trp Val Gln Lys Lys Arg Pro Gly Thr Ala Ala

Ala Gln Ala Ala Glu Ala Ala Gln Asn Val His Asn Gln Glu Gly

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355

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ctt Leu	cct Pro	gca Ala	acg Thr	aag Lys 10	aca Thr	att Ile	cca Pro	aag Lys	gag Glu 15	ctt Leu	ctt Leu	cct Pro	gta Val	gtt Val 20	gat Asp	163
	ccg Pro															211
	cgg Arg		_				_	_			-					259
	ttc Phe 55								_				_			307
_	act Thr	_		-			-	_	_	_	_	-	_		_	355
	gtt Val															403
	ctt Leu															451
	ctg Leu															499
	gaa Glu 135															547
	gct Ala	-	-	_	_					_		_			_	595
	gat Asp															643
-	gaa Glu	_				-	_	_					_	_	_	691
	cgt Arg															739
	cct Pro 215		_			_	_				_	_		_		787
	atc Ile															835
cgc	cat	gac	ctt	ggt	aat	cca	gct	ggg	tac	att	cct	gct	gtt	gtg	tac	883

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Arg	His	Asp	Leu	Gly 250	Asn	Pro	Ala	Gly	Tyr 255	Ile	Pro	Ala	Val	Val 260	Tyr
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aca															
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Leu	Pro	Val	Val 20	Asp	Thr	Pro	Gly	Ile 25	Glu	Leu	Val	Ala	Lys 30	Glu	Ala
Ala	Asp	Leu 35	Gly	Ala	Thr	Arg	Leu 40	Ala	Ile	Ile	Thr	Ala 45	Pro	Asn	Lys
Asp	Gly 50	Ile	Leu	Lys	His	Phe 55	Glu	Glu	Phe	Pro	Glu 60	Leu	Glu	Ala	Thr
Leu 65	Glu	Ala	Arg	Gly	Lys 70	Thr	Asp	Gln	Leu	Asn 75	Lys	Val	Arg	Ala	Ala 80
Arg	Glu	Leu	Ile	Ala 85	Thr	Val	Pro	Val	Val 90	Gln	Glu	Lys	Pro	Leu 95	Gly
Leu	Gly	His	Ala 100	Val	Gly	Leu	Ala	Glu 105	Ser	Val	Leu	Asp	Asp 110	Asp	Glu
Asp	Val	Val 115	Ala	Val	Met	Leu	Pro 120	Asp	Asp	Leu	Val	Leu 125	Pro	Phe	Gly
Val	Thr 130	Glu	Arg	Met	Ala	Glu 135	Val	Arg	Ala	Lys	Phe 140	Gly	Gly	Ser	Val
Leu 145	Ala	Ala	Ile	Glu	Val 150	Ala	Glu	Asp	Glu	Val 155	Ser	Asn	Tyr	Gly	Val 160
Phe	Lys	Leu	Gly	Glu 165	Leu	Asp	Ala	Glu	Ser 170	Glu	Ser	Glu	Gly	Ile 175	Arg
Arg	Val	Val	Gly 180	Met	Val	Glu	Lys	Pro 185	Ala	Pro	Glu	Asp	Ala 190	Pro	Ser
Arg	Phe	Ala 195	Ala	Thr	Gly	Arg	Tyr 200	Leu	Leu	Asp	Arg	Ala 205	Ile	Phe	Asp

Ala Leu Arg Arg Ile Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr 210 215 220

931

978

Asp Ala Ile Ala Leu Leu Ile Glu Glu Gly His Pro Val His Ile Val 225 230 235 240

Val His Glu Gly Lys Arg His Asp Leu Gly Asn Pro Ala Gly Tyr Ile 245 250 255

Pro Ala Val Val Tyr Phe Gly Leu Arg His Ala Glu Tyr Gly Ser Lys 260 265 270

Ile His Arg Ala Val Lys Glu Ile Leu Ala Glu Phe Glu Ser 275 280 285

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<211> 526

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

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<223> RXA02028

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Met Ser Leu Pro Ile

1 5

gat gag cac gtg aac gcg gtt aaa acc gtc gta gtg cct gct gca gga 163 Asp Glu His Val Asn Ala Val Lys Thr Val Val Val Pro Ala Ala Gly 10 15 20

ctg gga acc cga ttc ctt ccg gcc acc aaa acc gta ccc aag gag ttg 211 Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Val Pro Lys Glu Leu 25 30 35

ctg ccg gtt gtc gat acc cca ggt att gag ctg att gct gct gag gct 259 Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Ile Ala Ala Glu Ala 40 45 50

gcc gaa ctt ggt gcg acc agg ctg gcg atc atc act gcg cca aac aaa 307 Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys 55 60 65

gct ggg gta ctt gca cac ttt gag cgt tct tct gaa ttg gaa gaa acg 355
Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser Glu Leu Glu Glu Thr
70 75 80 85

ctg atg gag cgt ggc aag act gac cag gtg gag ata atc cgc cgc gcc 403 Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu Ile Ile Arg Arg Ala 90 95 100

gcc gat tta atc aag gca gtt cca gta acc cag gac aag ccg ctg ggg 451 Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln Asp Lys Pro Leu Gly 105 110 115

cta ggt cat gct ggt ttg gct gag tct gtg ttg gat gat gat gaa 499 Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Glu

120 125 130 526 gat gtc gta gcg gtg atg ttg ccg cac Asp Val Val Ala Val Met Leu Pro His 135 140 <210> 270 <211> 142 <212> PRT <213> Corynebacterium glutamicum <400> 270 Met Ser Leu Pro Ile Asp Glu His Val Asn Ala Val Lys Thr Val Val Val Pro Ala Ala Gly Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Val Pro Lys Glu Leu Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Ile Ala Ala Glu Ala Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser Glu Leu Glu Glu Thr Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu Ile Ile Arg Arg Ala Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln Asp Lys Pro Leu Gly Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Glu Asp Val Val Ala Val Met Leu Pro His 135 <210> 271 <211> 1284 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1261) <223> RXA01262 <400> 271 tatactcgtc aagggccttc gataaaacaa agacaatttt cccccgacgg gacaatctga 60 aaacttgctg tatcaataaa acacgaaaag gaatactttt atg aaa att gcc gtc 115 Met Lys Ile Ala Val gca ggg ctc gga tat gtt ggg ctt tca aat gca gct ctc ctc tct aaa 163 Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala Ala Leu Leu Ser Lys 10 15

						gtt Val										211
_		_		_	_	cca Pro		_	_	_	_		_	-		259
						aac Asn 60										307
						ttt Phe										355
						t.tt Phe										403
						tct Ser										451
			_			aca Thr	_	_		_		_			-	499
						cct Pro 140										547
	-					tcc Ser	_	_	_	_		_	_	_		595
						act Thr	_		_			-		-	_	643
	_				_	gac Asp				_						691
						gca Ala										739
						cga Arg 220										787
						cgt Arg										835
						tgt Cys		_		-	_		_			883

Ala Asn Tyr Lys 265	gat gtc (Asp Val	Pro Gln							931
gca aat aag act Ala Asn Lys Thr 280									979
tca cct act gta Ser Pro Thr Val 295	Val Gly								1027
gat aac ttt cgt Asp Asn Phe Arg 310									1075
gcc aag gga atc Ala Lys Gly Ile									1123
act ttc tac aat Thr Phe Tyr Asn 345		Ile Leu	_	_			_	_	1171
tac tgc gac atc Tyr Cys Asp Ile 360									1219
gta cca gaa aaa Val Pro Glu Lys 375	Val Tyr '	_	-	_	-	-			1261
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Ile Val Ile Lys Ser Thr Ile Pro Val Gly Phe Thr Ser Glu Leu Arg 125

Ile Lys His Pro Glu Ala Ser Ile Ile Phe Ser Pro Glu Phe Leu Arg 130

- 389 -

Glu Gly Arg Ala Phe Tyr Asp Asn Leu Tyr Pro Ser Arg Val Val 145 150 155 160

Gly Asp Arg Ser Pro Leu Gly Glu Glu Phe Ala Thr Leu Leu Ala Glu 165 170 175

Gly Ala Lys Glu Lys Pro Pro Ile Leu Leu Thr Asp Ser Thr Glu Ala 180 185 190

Glu Ala Ile Lys Leu Phe Ser Asn Thr Tyr Leu Ala Leu Arg Val Ala 195 200 205

Phe Phe Asn Glu Leu Asp Thr Tyr Ala Ser Val Arg Ser Leu Asp Thr 210 215 220

Lys Gln Ile Ile Glu Gly Val Gly Leu Asp Pro Arg Ile Gly Ser His 225 230 235 240

Tyr Asn Asn Pro Ser Phe Gly Tyr Gly Gly Tyr Cys Leu Pro Lys Asp 245 250 255

Thr Lys Gln Leu Leu Ala Asn Tyr Lys Asp Val Pro Gln Asn Leu Ile 260 265 270

Ser Ala Val Val Gln Ala Asn Lys Thr Arg Lys Asp Phe Ile Ala Glu 275 280 285

Asp Ile Leu Ser Lys Ser Pro Thr Val Val Gly Ile Tyr Arg Leu Val 290 295 300

Met Lys Ser Gly Ser Asp Asn Phe Arg Ser Ser Ser Ile Gln Gly Val 305 310 315 320

Met Lys Arg Ile Lys Ala Lys Gly Ile Glu Ile Val Val Phe Glu Pro 325 330 335

Asn Leu Gly Glu Glu Thr Phe Tyr Asn Ser Lys Ile Leu Asn Asp Ile 340 345 350

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Asp Glu Leu Ser Asp Val Pro Glu Lys Val Tyr Thr Arg Asp Ile Phe 370 375 380

Gln Arg Asp 385

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Ser Val Gl	-	Thr Phe	Pro Gl 205	n Leu	Leu G	Glu Glu 210		Lys	Arg	
gtc ttc gg Val Phe Gl 215					Arg A					787
agc gac tt Ser Asp Ph 230										835
tcc cca tt Ser Pro Le		Gly Lys								883
gcc ggc gt Ala Gly Va			_	eu Leu			-	_		931
cgc ggc ac Arg Gly Th 28	ır Glu Ile			_		-	Thr	_		979
ttc gac go Phe Asp Gl 295					Val I					1027
att tcc tc Ile Ser Se 310		_							_	1075
atc att go Ile Ile Gl		Ala Gln								1123
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Pro Met Le	eu Pro Thr 85	Ala Gly	His Pr 40	o Phe	Leu I	Thr His 45		Leu	Ala	

Arg Ile Lys Ala Ala Gly Ile Thr His Val Val Leu Gly Thr Ser Phe 50 55 60

Lys Ala Glu Val Phe Glu Glu Tyr Phe Gly Asp Gly Ser Glu Met Gly 65 70 75 80

Leu Glu Ile Glu Tyr Val Val Glu Asp Gln Pro Leu Gly Thr Gly Gly
85 90 95

Gly Ile Arg Asn Val Tyr Asp Lys Leu Arg His Asp Thr Ala Ile Val 100 105 110

Phe Asn Gly Asp Val Leu Ser Gly Ala Asp Leu Asn Ser Ile Leu Asp 115 120 125

Thr His Arg Glu Lys Asp Ala Asp Leu Thr Met His Leu Val Arg Val 130 135 140

Ala Asn Pro Arg Ala Phe Gly Cys Val Pro Thr Asp Glu Asp Gly Arg 145 150 155 160

Val Ser Glu Phe Leu Glu Lys Thr Glu Asp Pro Pro Thr Asp Gln Ile 165 170 175

Asn Ala Gly Cys Tyr Val Phe Lys Lys Glu Leu Ile Glu Gln Ile Pro 180 185 190

Ala Gly Arg Ala Val Ser Val Glu Arg Glu Thr Phe Pro Gln Leu Leu 195 200 205

Glu Glu Gly Lys Arg Val Phe Gly His Val Asp Ala Ser Tyr Trp Arg 210 215 220

Asp Met Gly Thr Pro Ser Asp Phe Val Arg Gly Ser Ala Asp Leu Val 225 230 235 240

Arg Gly Ile Ala Tyr Ser Pro Leu Leu Glu Gly Lys Thr Gly Glu Ser 245 250 255

Leu Val Asp Ala Ser Ala Gly Val Arg Asp Gly Val Leu Leu Gly 260 265 270

Gly Thr Val Val Gly Arg Gly Thr Glu Ile Gly Ala Gly Cys Arg Val 275 280 285

Asp Asn Thr Val Ile Phe Asp Gly Val Thr Ile Glu Pro Gly Ala Val 290 295 300

Ile Glu Asn Ser Ile Ile Ser Ser Gly Ala Arg Ile Gly Ala Asn Ala 305 310 315 320

His Ile Ser Gly Cys Ile Ile Gly Glu Gly Ala Gln Val Gly Ala Arg 325 330 335

Cys Glu Leu Asn Ala Gly Met Arg Val Phe Pro Gly Val Val Ile Pro 340 345 350

Asp Ser Gly Ile Arg Phe Ser Ser Asp Gln 355 360

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ttg gaa aag cca gct gac cct ccg gga acc cct gat gat cct gac atg

Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro Asp Asp Pro Asp Met

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	aaa gat gat g Lys Asp Asp G 2			_	-
	atc att ccg t Ile Ile Pro T 235	_			-
	tcc gga aac a Ser Gly Asn I 250	_			_
Gly Tyr Trp	cgc gac gtc g Arg Asp Val G 265	-			
	att tcc gtg c Ile Ser Val H		Phe Asn Leu T		
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	aag ggt gct g Lys Gly Ala V		His Ala Ile L		
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Gln Tyr Lys Ser His Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn 65 70 75 80

Val Ser Gly Pro Thr Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln
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Arg Leu Gly Lys Arg Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln
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Ser Leu Asn Leu Ile Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe 115 120 125

Gly Ala Asp His Val Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu 130 135 140

His Ile Ala Ser Gly Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro 145 150 155 160

Arg Glu Glu Ala Thr Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly
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Asn Ile Thr Glu Phe Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro 180 185 190

Asp Asp Pro Asp Met Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr 195 200 205

Thr Glu Ala Leu Ile Gln Ala Leu Lys Asp Glu Asn Asn Glu Asn 210 215 220

Ser Asp His Asp Met Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg 225 230 235 240

Asn Asp Ala His Val Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala 245 250 255

Thr Glu Arg Asp Lys Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala 260 265 270

Phe Tyr Glu Cys His Met Asp Leu Ile Ser Val His Pro Ile Phe Asn 275 280 285

Leu Tyr Asn Ser Glu Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu 290 295 300

Pro Pro Ala Lys Phe Val Arg Gly Gly Ile Ala Gln Ser Ser Met Val 315 Ser Ser Gly Ser Ile Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu 325 330 Ser Asn Asn Val Val Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val 345 Leu Met Pro Gly Val Arg Ile Gly Lys Gly Ala Val Val Arg His Ala 355 360 Ile Leu Asp Lys Asn Val Val Val Arg Asp Gly Glu Leu Ile Gly Val 375 Asp Gln Val Arg Asp Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val 385 390 Val Val Gly Lys Asn Gln Val Val 405 <210> 277 <211> 903 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(880) <223> RXN00014 <400> 277 catcaaagtg accgccggcg gcgtcgaatg gtccgttgca ggaaacgcgg aagcagttag 60 tgagatetee gaaaetttaa gegeaetaga etaacaacae atg age aaa tat gea 115 Met Ser Lys Tyr Ala gac gat tta gcc tta gcc ctc gaa ctt gcc gaa ctt gcc gat tcc atc 163 Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu Leu Ala Asp Ser Ile 10 15 ace etc gae ege tte gaa gee tet gae etg gaa gta tee tee aag eea 211 Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu Val Ser Ser Lys Pro gac atq act ccc gtc agc gat gcc gac ctg gcg acc gaa gaa gca ctc 259 Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala Thr Glu Glu Ala Leu 40 45 cgt gag aaa atc gcc acc gcc cgc ccc gcc gac tcc atc ctc ggt gaa 307 Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp Ser Ile Leu Gly Glu 55 60 65 gaa ttc ggt ggc gac gta gaa ttc agc ggc cgc cag tgg atc atc gac 355 Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg Gln Trp Ile Ile Asp 70 75 80 8.5 ccc atc gac ggc acc aaa aac tac gtc cgc ggc gtc ccc gta tgg gca 403 Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly Val Pro Val Trp Ala

90 95 100 acc ctg atc gcg ctg ctc gac aac ggc aaa ccc gtc gca ggt gtc atc 451 Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro Val Ala Gly Val Ile 105 110 tcc gca ccc gca ctg gct agg cgt tgg tgg gca tcc gaa ggg gcc ggc 499 Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala Ser Glu Gly Ala Gly 120 125 gca tgg cgc acc ttc aac ggc agc tcc cca cgc aaa ctg tcc gtg tcc 547 Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg Lys Leu Ser Val Ser 135 140 cag gtg tcc aag ctt gac gac gcc tcc ctc tcc ttc tcc tcc ctc tcc 595 Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser Phe Ser Ser Leu Ser 150 155 ggc tgg gcc gaa cga gat ttg cgc gat cag ttc gtc tcc cta act gat 643 Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe Val Ser Leu Thr Asp 170 acc acc tgg cga ctc cgc ggc tac ggc gac ttc ttc tcc tac tgc ctc 691 Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe Phe Ser Tyr Cys Leu 185 190 gtc gcc gaa ggt gcc gtc gat atc gcc gct gaa cca gaa gtc agc ctc 739 Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu Pro Glu Val Ser Leu 200 205 tgg gat ctt gct ccc ctg tcc atc ctg gtc acc gaa gcc gga gga aag 787 Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr Glu Ala Gly Gly Lys 215 220 ttc acc tca ctg gct ggc gtc gat gga cca cac ggt ggc gat gca gta 835 Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His Gly Gly Asp Ala Val 235 gcc acc aac ggc atc ctg cac gat gag acg ctg gat cgt tta aaa 880 Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu Asp Arg Leu Lys tagactcccg ggttttgctt ggt 903 <210> 278 <211> 260 <212> PRT <213> Corynebacterium glutamicum <400> 278 Met Ser Lys Tyr Ala Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu 10 Leu Ala Asp Ser Ile Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu 20 Val Ser Ser Lys Pro Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala 40

Thr Glu Glu Ala Leu Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp

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Gln	Trp	Ile	Ile	Asp 85	Pro	Ile	Asp	Gly	Thr 90	Lys	Asn	Tyr	Val	Arg 95	Gly	
Val	Pro	Val	Trp 100	Ala	Thr	Leu	Ile	Ala 105	Leu	Leu	Asp	Asn	Gly 110	Lys	Pro	
Val	Ala	Gly 115	Val	Ile	Ser	Ala	Pro 120	Ala	Leu	Ala	Arg	Arg 125	Trp	Trp	Ala	
Ser	Glu 130	Gly	Ala	Gly	Ala	Trp 135	Arg	Thr	Phe	Asn	Gly 140	Ser	Ser	Pro	Arg	
Lys 145	Leu	Ser	Val	Ser	Gln 150	Val	Ser	Lys	Leu	Asp 155	Asp	Ala	Ser	Leu	Ser 160	
Phe	Ser	Ser	Leu	Ser 165	Gly	Trp	Ala	Glu	Arg 170	Asp	Leu	Arg	Asp	Gln 175	Phe	
Val	Ser	Leu	Thr 180	Asp	Thr	Thr	Trp	Arg 185	Leu	Arg	Gly	Tyr	Gly 190	Asp	Phe	
Phe	Ser	Tyr 195	Суѕ	Leu	Val	Ala	Glu 200	Gly	Ala	Val	Asp	Ile 205	Ala	Ala	Glu	
Pro	Glu 210	Val	Ser	Leu	Trp	Asp 215	Leu	Ala	Pro	Leu	Ser 220	Ile	Leu	Val	Thr	
Glu 225		Gly	Gly	Lys	Phe 230	Thr	Ser	Leu	Ala	Gly 235	Val	Asp	Gly	Pro	His 240	
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tga	gatc	tcc ç	gaaac	ettta	aa go	egcad	ctaga	a cta	agcaa	acac	_	agc Ser			_	115
		tta Leu														163

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Thr Glu Glu Ala Leu Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp 50 55 60

Ser Ile Leu Gly Glu Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg 65 70 75 80

Gln Trp Ile Ile Asp Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly 85 90 95

Val Pro Val Trp Ala Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro 100 105 110

Val Ala Gly Val Ile Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala 115 120 125

Ser Glu Gly Ala Gly Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg 130 135 140

Lys Leu Ser Val Ser Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser 145 150 155 160

Phe Ser Ser Leu Ser Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe 165 170 175

Val Ser Leu Thr Asp Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe 180 185 190

Phe Ser Tyr Cys Leu Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu 195 200 205

Pro Glu Val Ser Leu Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr 210 215 220

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                                             Val Lys Gly Ile Ile
ctc gca ggt ggc tcc ggc acc cgg ctc tac ccc atc acc aag ggc atc
                                                                   163
Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro Ile Thr Lys Gly Ile
tcc aag caa ctg atg ccg att tac gac aaa ccc atg gtc tac tac cca
                                                                   211
Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro Met Val Tyr Tyr Pro
                                                                   259
ctg acc acg ctc att cag gcc ggc atc aaa gac atc ctg att atc acc
Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp Ile Leu Ile Ile Thr
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acc cct gaa gac agc gcc tcc ttt gaa cgc ttg ctt ggc gac ggc tcc
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Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu Leu Gly Asp Gly Ser
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tcc tgg ggc atc aac ctc acc tac gcc gtc caa ccc tcc ccc gac gga
                                                                   355
Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln Pro Ser Pro Asp Gly
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cta gcc caa gca ttc atc ggc gag gaa ttc atc ggt gac gac gac
                                                                   403
Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe Ile Gly Asp Asp Asp
gtc gcg ttg gtg ctt ggc gat aac atc ttc gac ggc gca caa ctt ggc
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Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp Gly Ala Gln Leu Gly
cac qca cta aag cag tgc tcc aac ccc gac ggt ggc att gtc ttt gct
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His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly Gly Ile Val Phe Ala
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tat gag gtc tcc gat cct gag cgt tat ggc gtg gta gta ttt gat gct
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Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val Val Glu Phe Asp Ala
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gct aat aag gcg gtg tct att gaa gaa aag ccc acc gcg cca aaa tcc
                                                                   595
Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro Thr Ala Pro Lys Ser
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                                        160
aac ttt gcc gtg gta gga cta tat ttc tac gac aat cgc gtg gtg gac
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Asn Phe Ala Val Val Gly Leu Tyr Phe Tyr Asp Asn Arg Val Val Asp
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ctg gad Leu Ası 21	Arg														787
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Gly Ala Gln Leu Gly His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly 115 120 125

Gly Ile Val Phe Ala Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val

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tctt	gaco	gat o	ctgaç	gctto	cg ad	cgaco	gaaga	a tta	agaco	geee	-	tcg Ser			=	115
							gcg Ala									163
						_	ttc Phe	-	-	_	-	_	_			211
		_	_			_	atg Met 45				_	-	_	_	_	259
							gac Asp									307

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Glu Ser Val Asp Glu Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr 50 55 60

Tyr Ala Arg Asp Leu Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu 65 70 75 80

Gly Val Arg Val Arg Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser 85 90 95

Val Trp Ala Gly Leu Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp 100 105 110

Ala Ile Val Leu Ile His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly 115 120 125

Met Ile Ala Arg Val Val Arg Lys Val His Glu Gly Ala Thr Ala Val 130 135 140

Ile Pro Val Leu Pro Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp 145 150 155 160

Gly Gly Val Val Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val 165 170 175

Gln Thr Pro Gln Gly Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu 180 185 190

Lys Phe Phe Ala Asp Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala 195 200 205

Ser Leu Met Glu Trp Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp 210 215 220

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Gly Glu Ile Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu 230 235 240 245	835
acc tct gac cgc cag ctg cac acc ctc gtg gcc act gcg gca ggt tcc Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser 250 255 260	883
aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg 265 270 275	931
agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro 280 285 290	979
gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg 295 300 305	1027
act cac taggggaaaa tccaccacaa atc Thr His 310	1056
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1 5 10 15 Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn 20 25 Ser Asp Ala Glu Ala Thr Gly 45 Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly 45 Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu	
1 5 10 15 Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn 20 25 Glu Val Val Val Val Ile Asp Asn 30 Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly 45 Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu 50 Che Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln	
1 5 10 15 Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn 20 25 Slu Val Val Val Val Ile Asp Asn 30 Slu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly 45 Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu 50 Slu Ser Val Val Ile Phe His Leu Ala Ala Gln 65 Slu Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr	
Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn 20 Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly 40 Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu 50 Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln 65 Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly	
Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn 20 Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly 45 Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu 50 Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln 65 Rap Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr 95 Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly 100 Val Arg Lys Val Val Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu	

Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val 165 170 Tyr Gly Pro Arg Gln Asp Pro His Gly Glu Ala Gly Val Val Ala Ile 185 Phe Ala Leu Arg Leu Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp 195 200 Gly Gly Asn Thr Arg Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala Phe Tyr Leu Ala Ser Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser Lys Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr 295 Val Glu Tyr Phe Arg Thr His 305 310 <210> 287 <211> 1134 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1111) <223> RXA01887 <400> 287 catctttaca ggaaacccct tgacggcatc aatgggtggt atctagtatc tactagaacg 60 ttatagtaga acgttctagt aaaacttgga aggatgaaaa atg tca gtc aaa ctt Met Ser Val Lys Leu gcc ctc atc ggt gct gga cgc atc gga tca aat cac gca cgc ctg atc 163 Ala Leu Ile Gly Ala Gly Arg Ile Gly Ser Asn His Ala Arg Leu Ile 10 aca aac cac gtg atc ggc tct gaa ctg gtc gcc gtc gtt gac cca act 211 Thr Asn His Val Ile Gly Ser Glu Leu Val Ala Val Val Asp Pro Thr 25 30

ccc aac gca gaa acc ctc gct gat gaa ttg ggc gcc gtt gcg ttc tct

Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly Ala Val Ala Phe Ser

45

40

259

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						cac His										355
						gtg Val										403
						aac Asn										451
						cgt Arg										499
						gat Asp 140										547
		_	_			cca Pro			_	_			_			595
_					_	gaa Glu					-		-		_	643
						gca Ala										691
						gaa Glu										739
						ttt Phe 220										787
_	-		_	_	-	tat Tyr			_	_	_		-	_		835
						acc Thr										883
						ggc Gly										931
						gct Ala										979
gac	tcc	atc	cgt	acc	aac	acc	cct	tcc	aag	gtt	сса	ggc	gaa	gct	gca	1027

Asp	Ser 295	Ile	Arg	Thr	Asn	Thr 300	Pro	Ser	Lys	Val	Pro 305	Gly	Glu	Ala	Ala	
_		_				-	ctc Leu		_		_	_	_	_		1075
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<210> 288 <211> 337 <212> PRT <213> Corynebacterium glutamicum

<400> 288

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His Ala Arg Leu Ile Thr Asn His Val Ile Gly Ser Glu Leu Val Ala 20 25 30

Val Val Asp Pro Thr Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly 35 40 45

Ala Val Ala Phe Ser Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile
50 55 60

Asp Ala Val Leu Ile Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val 65 70 75 80

Val Lys Ala Ala Ala Gly Lys His Val Phe Val Glu Lys Pro Met 85 90 95

Ala Val Thr Leu Glu Asp Ala Asp Arg Ala Ile Asn Ala Arg Glu 100 105 110

Ala Asn Thr Val Leu Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly 115 120 125

Phe Ala Ala Arg Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro 130 135 140

Gln Leu Leu Arg Ser Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp 145 150 155 160

Pro Asn Lys Ile Pro Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His 165 170 175

Asp Phe Asp Ala Leu Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu 180 185 190

Val Thr Ala His Ala Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr 195 200 205

Gly Phe Leu Asp Thr Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala 210 215 220

Ile Gly Thr Ala Glu Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val 225 230 235 Arg Gly Glu Val Phe Gly Ser Lys Gly Met Met Thr Ala Gly Asp Ala 250 Arg Ala Thr Asn Met Thr Phe Tyr Gly Ala Glu Gly Ile Ala Ala Ala 265 Thr Ser Arg Ala Asp Thr Asp Leu Ser Asp Ala Tyr Arg Ala Glu Phe Gln Ala Phe Val Asp Ser Ile Arg Thr Asn Thr Pro Ser Lys Val 295 Pro Gly Glu Ala Ala Arg Thr Ala Leu Leu Ile Ala Leu Gly Ala Ile 310 315 Arg Ser Val Glu Thr Gly Ala Thr Ile Asn Leu Ala Glu Ser Ile Glu 330 Val <210> 289 <211> 996 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(973) <223> RXN00013 <400> 289 ctgcagaaaa ttcgggacgc atgattgcac atattacccg caccgattgt gattcttaga 60 acgccacctt attcagcaca cttggccgac ggcatgcaca atg gaa ggc atg act Met Glu Gly Met Thr aat cca gag cag aca cat ccc gct gca agc ctc gaa gac atg atc aaa 163 Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu Glu Asp Met Ile Lys 10 15 acc atc aca aag acc ttc gtg att gct cac gat cag gat tct gat gag 211 Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp Gln Asp Ser Asp Glu 25 30 cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc 259 His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly Arg Leu Ala Trp Arg 40 45 50 307 atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys Thr Ser Val Ser Asp 55 60 gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt 355 Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala Phe Val Ala Gly Val

70					75				80					85	
												gaa Glu			403
-			-		_				_		-	ccg Pro 115	_	-	451
												tcg Ser			499
	_	_			_				_	_		ctt Leu			547
_	-		_		_	_		_				ggc Gly	_		595
	_		_		-		_		_	-		gtc Val	-	_	643
						_	_				_	tca Ser 195	_		691
												acc Thr			739
_	_	_	-	_			-			_	-	gcc Ala			787
												gca Ala			835
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<213> Corynebacterium glutamicum

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Glu Asp Met Ile Lys Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp
20 25 30

Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly $35 \hspace{1cm} 40 \hspace{1cm} 45$

Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys
50 55 60

Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala 65 70 75 80

Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu 85 90 95

Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val 100 105 110

Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr 115 120 125

Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser 130 135 140

Arg Val Leu Phe Gly Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp 145 150 155 160

Phe Gly Gly Pro Gly Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp 165 170 175

Leu Leu Val Asp Ala Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile 180 185 190

His Pro Ser Arg Ile Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser 195 200 205

Val Ala Thr His Pro Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile 210 215 220

Asp Leu Ala Asn Ile Ala Asp Gly Ser Met Gly Ala Trp Val Gln His 225 230 235 240

Ser Val Ala Asp Trp Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly 245 250 255

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Ala Leu Asp 290

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175

691

ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc

BGI-126CP - 415 -

Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile His Pro Ser Arg Ile 185 190 195	
gcg gaa cct gat att caa aag gcg tgg atg agc gtt gcc acc cac cct Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro 200 205 210	739
gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile 215 220 225	787
gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp 230 235 240 245	835
gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gcg tgc Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys 250 255 260	883
atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala 265 270 275	931
gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser Ala Leu Asp 280 285 290	973
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Phe	Gly	Gly	Pro	Gly 165	Ile	Arg	Thr	Thr	Leu 170	Asp	Gly	Lys	Glu	Leu 175	Asp	
Leu	Leu	Val	Asp 180	Ala	Pro	Leu	Asn	Gln 185	Ile	Ser	Leu	Ala	Thr 190	Tyr	Ile	
His	Pro	Ser 195	Arg	Ile	Ala	Glu	Pro 200	Asp	Ile	Gln	Lys	Ala 205	Tṛp	Met	Ser	
Val	Ala 210	Thr	His	Pro	Ala	Thr 215	Leu	Arg	Met	Phe	Gly 220	Ala	Gly	Ser	Ile	
Asp 225	Leu	Ala	Asn	Ile	Ala 230	Asp	Gly	Ser	Met	Gly 235	Ala	Trp	Val	Gln	His 240	
Ser	Val	Ala	Asp	Trp 245	Asp	Trp	Leu	Pro	Gly 250	Arg	Ala	Leu	Ile	Glu 255	Gly	
Val	Gly	Gly	Ala 260	Cys	Ile	Lys	Val	Thr 265	Ala	Gly	Gly	Val	Glu 270	Trp	Ser	
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cgaa	agago	gct t	tgg	ctgca	ag ta	agaaa	aagct	cg(gttaa	atac	_	_	gct Ala	_		115
						gcc Ala										163
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						atg Met										259

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					cgc Arg 75											355
					aac Asn											403
_	_	_	_		gtc Val	_					_		_	_		451
					ttt Phe											499
					caa Gln											547
					tcc Ser 155											595
_		_		_	acc Thr			_	_	_			-		-	643
					ggt Gly								_			691
				-	tcg Ser		_			-		_			-	739
					cgc Arg											787
					cca Pro 235											835
					tta Leu											883
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<212> PRT

<213> Corynebacterium glutamicum

<400> 294

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Ala Glu Ala Leu Phe Met Gln Gly Phe Gly Ala Ala Pro Ala His Met $20 \hspace{1cm} 25 \hspace{1cm} 30$

Lys Ser Pro Gly Asp Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser 35 40 45

His Met Arg Ser Met Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly 50 60

Glu Glu Gly Gly Gly Ala Thr Ser Gly Thr Arg Trp Val Ile Asp Pro 65 70 75 80

Ile Asp Gly Thr Ala Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile 85 90 95

Leu Val Ser Leu Leu Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser 100 105 110

Met Pro Met Leu Gly Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu 115 120 125

Met Ile Asn Gly Glu Pro Gln Glu Pro Leu Gln Glu Gln Ser Ser Leu 130 135 140

Val Ser His Ile Gly Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala 145 150 155 160

Phe Pro Val Glu Leu Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser 165 170 175

Tyr Leu Arg Pro Arg Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe 180 185 190

Thr Ala Gln Gly Ile Phe Gly Ala Cys Val Ser Phe Ser Pro His Val 195 200 205

Trp Asp Asn Ser Ala Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln 210 215 220

Val Thr Asp Thr Glu Gly His Pro Trp Ala Pro Gly Arg Gly Val Val 225 230 235 240

Ala Gly Thr Lys Arg Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys 245 250 255

Val Arg Leu Met His Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu 260 265 270

Glu Tyr Lys 275

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<223> RXN01332
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gca gaa gac gcg ccg ggt gca cag gcc ttc act cgc att gaa gat gct
Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala
             20
atc gca gcc gat gct gtc gac gca gtg ctg atc gcc gta cca ggt cag
                                                                   144
Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln
ttc cat gag cca gta ctt gtc cca gca cta gaa gca ggc ctt ccc atc
                                                                   192
Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile
ctg tgt gaa aag cca ctg acc cca gat tct gaa tcc tca ctg cgc atc
                                                                   240
Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile
gtc gag ctg gag cag aag ctg gac aag cca cac atc cag gtt ggt ttc
                                                                   288
Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe
                 8.5
atg cgc cgc ttc gac cct gag tac aac aac ttg cgc aaa ttg gtg gaa
                                                                   336
Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu
tcc ggc gaa gct ggc gaa ctg ctc atg ctc cgc ggc ctg cac cgc aac
                                                                   384
Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn
        115
cca agt gtt ggt gag agc tac acc cag tcc atg ctg atc acc gac tcc
                                                                   432
Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser
                        135
gtc gtc cac gaa ttc gat gtc atc cca tgg ctc gca ggc tcc cga gtt
                                                                   480
Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val
gtc tcc gtt gaa gtg aag tac cca aag acc tcc tca ctg gcg cac tcc
                                                                   528
Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser
ggc ctc aag gaa cca atc ctg gtg atc atg gag ctc gaa aac ggc gtg
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Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val
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<210> 296 <211> 192

<212> PRT

<213> Corynebacterium glutamicum

<400> 296

His Ile Ser Ala Ile Ile Glu Pro Asp Ala Ala Arg Ala Ala Ala 1 5 10 15

Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala 20 25 30

Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln 35 40 45

Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile 50 55 60

Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile 65 70 75 80

Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe 85 90 95

Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu 100 105 110

Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn 115 120 125

Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser 130 135 140

Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val 145 150 155 160

Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser 165 170 175

Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val 180 185 190

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(549)

<223> FRXA01332

<400> 297

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ttc act cgc att gaa gat gct atc gca gcc gat gct gtc gac gca gtg 96 Phe Thr Arg Ile Glu Asp Ala Ile Ala Ala Asp Ala Val Asp Ala Val

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					ccc Pro											192
					cgc Arg 70											240
				-	ggt Gly											288
					gtg Val											336
	_		_		cgc Arg			_	_			_			_	384
	_	_			gac Asp		_	-		_		-	_			432
		_			cga Arg 150	_	_		_	_	Val	_			_	480
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_			_		ggc Gly											549
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Phe	Thr	Arg	Ile 20	Glu	Asp	Ala	Ile	Ala 25	Ala	Asp	Ala	Val	Asp 30	Ala	Val	
Leu	Ile	Ala 35	Val	Pro	Gly	Gln	Phe 40	His	Glu	Pro	Val	Leu 45	Val	Pro	Ala	
Leu	Glu 50	Ala	Gly	Leu	Pro	Ile 55	Leu	Cys	Glu	Lys	Pro 60	Leu	Thr	Pro	Asp	

Ser Glu Ser Ser Leu Arg Ile Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe Met Arg Arg Phe Asp Pro Glu Tyr Asn 85 90 Asn Leu Arg Lys Leu Val Glu Ser Gly Glu Ala Gly Glu Leu Leu Met Leu Arg Gly Leu His Arg Asn Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser Val Val His Glu Phe Asp Val Ile Pro 135 Trp Leu Ala Gly Ser Arg Val Val Ser Val Glu Val Lys Tyr Pro Lys 150 Thr Ser Ser Leu Ala His Ser Gly Leu Lys Glu Pro Ile Leu Val Ile 165 170 Met Glu Leu Glu Asn Gly Val 180 <210> 299 <211> 1128 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1105) <223> RXA01632 <400> 299 aagggctgca acgtgctttc gacaccacca tcgcagcgtt tgaacaagct gctcgtctcg 60 ccccctccac taactgatct ttgaaaggct gaaaaaactc atg act ctt cgt atc 115 Met Thr Leu Arg Ile gcc ctt ttc ggc gct ggc cgc atc ggt cac gtc cac gct gcc aac att 163 Ala Leu Phe Gly Ala Gly Arg Ile Gly His Val His Ala Ala Asn Ile gct gca aac cct gat ctt gaa ctc gtt gtt atc gcc gat cct ttc att 211 Ala Ala Asn Pro Asp Leu Glu Leu Val Val Ile Ala Asp Pro Phe Ile gaa ggc gca cag cgt ttg gca gaa gcc aat ggg gca gaa gcg gtt gca 259 Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly Ala Glu Ala Val Ala 45 tca cca gat gag gtg ttc gcc cgc gat gat atc gat ggc atc gtg atc 307 Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile Asp Gly Ile Val Ile 60 ggt tca cca acc agc acc cac gtt gat ctg atc acc cgc gcc gtg gaa 355 Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile Thr Arg Ala Val Glu 75 80

							gaa Glu								403
_		_	-	_			aag Lys			_		-		_	 451
_	_				_	_	ttc Phe 125	_				_	_		499
	_		-		_		atc Ile			-		_	_		547
	_	_	_				gca Ala	_	_	_			_		595
							acc Thr								643
							gaa Glu								691
							ttc Phe 205								739
							gag Glu								787
							cag Gln								835
							atc Ile								883
							gca Ala								931
	_		_	_	_		aag Lys 285	_			_			_	979
							ttc Phe								1027
							gca Ala								1075

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cct																
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	His	Ala	Ala	Asn 20	Ile	Ala	Ala	Asn	Pro 25	Asp	Leu	Glu	Leu	Val 30	Val	Ile
	Ala	Asp	Pro 35	Phe	Ile	Glu	Gly	Ala 40	Gln	Arg	Leu	Ala	Glu 45	Ala	Asn	Gly
	Ala	Glu 50	Ala	Val	Ala	Ser	Pro 55	Asp	Glu	Val	Phe	Ala 60	Arg	Asp	Asp	Ile
	Asp 65	Gly	Ile	Val	Ile	Gly 70	Ser	Pro	Thr	Ser	Thr 75	His	Val	Asp	Leu	Ile 80
	Thr	Arg	Ala	Val	Glu 85	Arg	Gly	Ile	Pro	Ala 90	Leu	Cys	Glu	Lys	Pro 95	Ile
	Asp	Leu	Asp	Ile 100	Glu	Met	Val	Arg	Ala 105	Cys	Lys	Glu	Lys	Ile 110	Gly	Asp
	Gly	Ala	Ser 115	Lys	Val	Met	Leu	Gly 120	Phe	Asn	Arg	Arg	Phe 125	Asp	Pro	Ser
	Phe	Ala 130	Ala	Ile	Asn	Ala	Arg 135	Val	Ala	Asn	Gln	Glu 140	Ile	Gly	Asn	Leu
	Glu 145	Gln	Leu	Val		Ile 150		_	Asp				Ala	Pro		Asp 160
	Tyr	Ile	Ala	Gly	Ser 165	Gly	Gly	Ile	Phe	Arg 170	Asp	Met	Thr	Ile	His 175	Asp
	Leu	Asp	Met	Ala 180	Arg	Phe	Phe	Val	Pro 185	Asn	Ile	Val	Glu	Val 190	Thr	Ala
	Thr	Gly	Ala 195	Asn	Val	Phe	Ser	Gln 200	Glu	Ile	Ala	Glu	Phe 205	Asn	Asp	Tyr
	Asp	Gln 210	Val	Ile	Val	Thr	Leu 215	Arg	Gly	Ser	Lys	Gly 220	Glu	Leu	Ile	Asn
	Ile 225	Val	Asn	Ser	Arg	His 230	Cys	Ser	Tyr	Gly	Tyr 235	Asp	Gln	Arg	Leu	Glu 240
	7.7	Dl.	C1 -	0	T	61 -	14 - 4	.	7.7.	7.1 .	70	7	т1.	7	Desc	mh

Ala Phe Gly Ser Lys Gly Met Leu Ala Ala Asp Asn Ile Arg Pro Thr

Thr Val Arg Lys His Asn Ala Glu Ser Thr Glu Gln Ala Asp Pro Ile 260 265 270

Phe Asn Phe Phe Leu Glu Arg Tyr Asp Ala Ala Tyr Lys Ala Glu Leu 275 280 285

Ala Thr Phe Ala Gln Gly Ile Arg Asp Gly Gln Gly Phe Ser Pro Asn 290 295 300

Phe Glu Asp Gly Val Ile Ala Leu Glu Leu Ala Asn Ala Cys Leu Glu 305 310 315 320

Ser Ala Gln Thr Gly Arg Thr Val Thr Leu Asn Pro Ala Asn Val 325 330 335

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<223> RXA01633

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atc gga atg gtc ggc gtc ggc cgc att ggc cgc atg cac gtc gcc aac 163
Ile Gly Met Val Gly Val Gly Arg Ile Gly Arg Met His Val Ala Asn
10 15 20

atg ctt gcc gtt gct gaa act ttg aag gaa cgc gac ctc aac att gag 211 Met Leu Ala Val Ala Glu Thr Leu Lys Glu Arg Asp Leu Asn Ile Glu 25 30 35

atc gtg ctc gca gac gca atg ccc ggt ttt gcg gag cag gtg ggc gcg 259
Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala Glú Gln Val Gly Ala
40 45 50

gac atg ggc gtg aag gcg gcg gca agc gtc gat aag ctt att gag gac 307 Asp Met Gly Val Lys Ala Ala Ala Ser Val Asp Lys Leu Ile Glu Asp 55 60 65

ggg gtg gat gcc ctt ttc att gcc acc agc acc gct ggc cac gtc gat 355 Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr Ala Gly His Val Asp 70 75 80 85

gtt ttg cgc aag ggc atc gcg gca aag ctg ccg atg ttc tgc gag aag 403 Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro Met Phe Cys Glu Lys 90 95 100

ccg atc gcg tcg gat gtg cct gag tcg ctg aac atc atc cgc gaa att 451
Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn Ile Ile Arg Glu Ile
105 110 115

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							cag Gln 125									499
							cga Arg									547
							gta Val									595
							ggt Gly									643
							tgg Trp									691
		_	_		_		aac Asn 205		_		_			_	-	739
	_		_				gcc Ala			_		_	_			787
							cgt Arg									835
							aaa Lys									883
							gcg Ala									931
							gcc Ala 285									979
							gag Glu									1027
							gtg Val									1075
							ggc Gly									1123
							gcg Ala									1171
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Val Pro Ser Ala 360

<210> 302

<211> 361

<212> PRT

<213> Corynebacterium glutamicum

<400> 302

Met Lys Asn Ile Thr Ile Gly Met Val Gly Val Gly Arg Ile Gly Arg
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Met His Val Ala Asn Met Leu Ala Val Ala Glu Thr Leu Lys Glu Arg 20 25 30

Asp Leu Asn Ile Glu Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala 35 40 45

Glu Gln Val Gly Ala Asp Met Gly Val Lys Ala Ala Ala Ser Val Asp 50 55 60

Lys Leu Ile Glu Asp Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr 65 70 75 80

Ala Gly His Val Asp Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro 85 90 95

Met Phe Cys Glu Lys Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn 100 105 110

Ile Ile Arg Glu Ile Asp Ala Ala Gly Ala Thr Val Gln Val Gly His
115 120 125

Gln Arg Arg Phe Asp Leu Gly Tyr Gln Glu Ala Lys Arg Arg Leu Asp 130 135 140

Ala Gly Asp Leu Gly Trp Leu His Ser Leu Lys Ala Val Ser Ser Asp 145 150 155 160

Ala Phe Pro Pro Pro Val Ser Tyr Cys Ala Thr Ser Gly Gly Leu Phe 165 170 175

Arg Asp Val Ser Leu His Asp Phe Asp Ile Ile Arg Trp Leu Thr Gly
180 185 190

Gln Asp Ile Val Glu Val Tyr Ala Lys Gly Ser Asn Asn Gly Asp Pro 195 200 205

Glu Ile Gly Ala Val Gly Asp Ile Asp Thr Gly Ala Ala Leu Leu Thr 210 215 220

Leu Ala Asp Gly Thr Leu Ala Thr Ala Ile Ala Thr Arg Tyr Asn Gly 235 230 235

Ala Gly His Asp Val Arg Leu Asp Val Met Gly Ser Lys Asp Ser Thr 245 250 255

Ile Val Gly Leu Asp Glu Lys Ser Ala Phe Ala Ser Ala Glu Glu Gly 260 265 270

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Ile Asp Phe Pro Thr Gly Glu Ser His Pro Thr Phe Ala Glu Arg Phe 280 Ala Asp Ala Tyr Lys Asn Glu Cys Ile Ala Phe Val Glu Leu Ile Leu 295 290 Gly Glu Arg Glu Asn Pro Cys Thr Pro Ala Asp Ala Val Ala Ala Ala 315 Ile Val Ala Asp Ala Ala Gln Leu Ser Leu Val Thr Gly Glu Pro Val 325 Lys Ile Pro Thr Val Arg Glu Ile Leu Glu Gly Ser Ala Gln Pro Val Glu Val Arg Ala Leu Val Pro Ser Ala 355 <210> 303 <211> 1146 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1123) <223> RXN01406 <400> 303 qttcctcatt cctctaatcq qcqcactatc tttqcctcqc qacqqcqqtq cccqagcctt 60 115 ttcctcctct tagaaaccca cttctgaaag gtataaaaac atg act att cga atc Met Thr Ile Arg Ile 163 gga ctc gtt ggc tac ggt gtc ggc ggc agg ctc ttt cac acc cct tac Gly Leu Val Gly Tyr Gly Val Gly Gly Arg Leu Phe His Thr Pro Tyr 10 atc caa gct tct acg cac tgc gaa tta gta ggc gta gtt gct cgt tcc 211 Ile Gln Ala Ser Thr His Cys Glu Leu Val Gly Val Val Ala Arg Ser 25 qaa qqc acc aaa qca qcc qtt qca qaa qat ctt cca gat gtt gcc atc 259 Glu Gly Thr Lys Ala Ala Val Ala Glu Asp Leu Pro Asp Val Ala Ile gtg gga tcg ctg aca gaa ctc ctc gaa ctg ggc gtc gat gca gtg gtg 307 Val Gly Ser Leu Thr Glu Leu Leu Glu Leu Gly Val Asp Ala Val Val ate tee ace cet cea gee acg ege egg gaa etg gee ttg gaa gea ate 355 Ile Ser Thr Pro Pro Ala Thr Arg Arg Glu Leu Ala Leu Glu Ala Ile aac gca ggt gtc gca gtg gtt gcc gat aaa ccg ttt gca cca tca gcc 403 Asn Ala Gly Val Ala Val Val Ala Asp Lys Pro Phe Ala Pro Ser Ala 95 qca qat qcc atg gaa ctt qtc qaa qcc gcc gaa aag gct gga gtg ctg 451

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Ala	Asp	Ala	Met 105	Glu	Leu	Val	Glu	Ala 110	Ala	Glu	Lys	Ala	Gly 115	Val	Leu	
ctc Leu	aac Asn	gtc Val 120	ttc Phe	cac His	aac Asn	agg Arg	cgc Arg 125	aac Asn	gac Asp	acc Thr	cac His	att Ile 130	gtc Val	acg Thr	gca Ala	499
					gaa Glu											547
					cct Pro 155											595
					ggc Gly					-	_		_	_		643
					tct Ser											691
					aac Asn				-			-			_	739
					cac His											787
					ttg Leu 235											835
		_		_	acc Thr					_			_			883
					tgg Trp											931
					ggc Gly											979
		_			gat Asp	_		_	_	_		_				1027
					gca Ala 315											1075
					agc Ser											1123
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<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 304

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Phe His Thr Pro Tyr Ile Gln Ala Ser Thr His Cys Glu Leu Val Gly 20 25 30

Val Val Ala Arg Ser Glu Gly Thr Lys Ala Ala Val Ala Glu Asp Leu 35 40 45

Pro Asp Val Ala Ile Val Gly Ser Leu Thr Glu Leu Glu Leu Gly 50 55 60

Val Asp Ala Val Val Ile Ser Thr Pro Pro Ala Thr Arg Arg Glu Leu 65 70 75 80

Ala Leu Glu Ala Ile Asn Ala Gly Val Ala Val Ala Asp Lys Pro 85 90 95

Phe Ala Pro Ser Ala Ala Asp Ala Met Glu Leu Val Glu Ala Ala Glu 100 105 110

Lys Ala Gly Val Leu Leu Asn Val Phe His Asn Arg Arg Asn Asp Thr
115 120 125

His Ile Val Thr Ala Leu Gly Ile Gln Glu Glu Leu Gly Ala Met Arg 130 135 140

Gly Leu Asp Leu Arg Leu Asp Leu Ile Glu Pro Asp Ser Leu Glu Ala 145 150 155 160

Gly Pro Glu Gly Gly Leu Leu Arg Asp Leu Gly Ser His Val Val Asp 165 170 175

Gln Thr Leu Val Leu Met Gly Pro Ala Thr Ser Val Thr Ala Gln Leu 180 185 190

Gly Ser Ile Asp Leu Pro Glu Gly Pro Thr Asn Ala Arg Phe Arg Ile 195 200 205

Val Leu Glu His Glu Ser Gly Ala Val Ser His Ile Ser Ala Ser Lys 210 215 220

Ile Asp Arg Leu Glu Ser Trp Glu Ile Arg Leu Val Gly Glu Arg Gly 225 230 235 240

Ser Tyr Val Ser Asn Tyr Thr Asp Val Gln Thr Val Ala Ile Lys Gln 245 250 255

Gly Leu Arg Pro Thr Asn Asp Arg Glu His Trp Gly Tyr Glu Ser Glu 260 265 270

Glu Arg Trp Gly Thr Leu Val Thr Asp Glu Gly Ser Lys Val Ile Pro 275 280 285 Ser Ala Gln Gly Asp Tyr Thr Arg Phe Tyr Asp Ala Phe Ala Leu Ala 290 295 300

Val Glu Asn Gly Gly Ala Gly Pro Val Pro Ala Arg Glu Gly Val Ala 305 310 315 320

Val Leu Lys Val Leu Asp Ala Val Ala Gln Ser Ala Ala Glu Lys Arg 325 330 335

Thr Ile Glu Leu Ser 340

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<211> 1200

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(1177)

<223> RXN01630

<400> 305

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ccagataaaa acctgcgggt tgcgttttag gagaattccc atg agt gat caa aaa 115

Met Ser Asp Gln Lys

1 5

att gtt gtt ggc ctg cta ggc atc acc cac ccg cat gcg tcg gcg cgg 163
Ile Val Val Gly Leu Leu Gly Ile Thr His Pro His Ala Ser Ala Arg
10 15 20

gtg cgt gcc ctc cgt gaa att gat ggg gta gag gtc gtc gcc gcc gcg 211 Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu Val Val Ala Ala Ala 25 30 35

gat act gat tcc cgc ctc cag tac ttc acc gac aaa tat gat gtt gaa 259
Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp Lys Tyr Asp Val Glu
40 45 50

ccc cgc gag atc gat gac gtc ttg aac gac gat cgc atc aac gcc atc 307
Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp Arg Ile Asn Ala Ile
55 60 65

atg gtt cac tcc aag agc aag gac atg gtc cct cac gcc aag cgc gcg 355
Met Val His Ser Lys Ser Lys Asp Met Val Pro His Ala Lys Arg Ala
70 85

ctc gcg gcc gga aaa tcc gtc gtc gtg gag aag ccc ggc ggg gga aca 403 Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys Pro Gly Gly Gly Thr 90 95 100

gtg gcg gat ctt gag gag ctc ctg gcc ctc aaa gaa gct gcc gat cct 451 Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys Glu Ala Ala Asp Pro 105 110 115

cag cga atc gtg cag gtc ggg tac aac gtc cgc ctg tct gaa tcg gtt 499 Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg Leu Ser Glu Ser Val 120 125 130

				ctt Leu		-							_	-	547
				ggc Gly 155											595
				gca Ala											643
				gca Ala											691
	_	_		cat His	_		_				-	-		-	739
				tcc Ser											7,87
				ggc Gly 235								_			835
_	_	-		gga Gly		_		_		_	-				883
				gta Val											931
-	 			tgg Trp		_	_					_		_	979
_	-			aaa Lys								_			1027
				gaa Glu 315											1075
				gcg Ala											1123
				tac Tyr											1171
aac Asn	c taagaggagc actccatgaa acc											1200			

<210> 306

<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 306

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His Ala Ser Ala Arg Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu
20 25 30

Val Val Ala Ala Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp 35 40 45

Lys Tyr Asp Val Glu Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp 50 55 60

Arg Ile Asn Ala Ile Met Val His Ser Lys Ser Lys Asp Met Val Pro 65 70 75 80

His Ala Lys Arg Ala Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys 85 90 95

Pro Gly Gly Gly Thr Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys 100 105 110

Glu Ala Ala Asp Pro Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg 115 120 125

Leu Ser Glu Ser Val Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu 130 135 140

Ile Gly Glu Val Val Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly 145 150 155 160

Glu His Ile Thr Glu His Leu Asn Gln Pro Ala Asp Met Gly Gly Val 165 170 175

Leu Trp Ile Leu Gly Cys His Met Leu Asp Ala Leu Val Glu Val Phe 180 185 190

Gly Ala Pro Glu Ser Val Asn Ala Arg Val His Lys Thr Ala Lys Leu 195 200 205

Ser Asp Asp Thr Ser Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr 210 215 220

Pro Asp Phe Ser Val Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu 225 230 235 240

Trp Phe Glu Ser Ser Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile 245 250 255

Glu Ala Gly Ile Leu Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser 260 265 270

Arg Gln Gly Trp Pro Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe 275 280 285

Ł

Thr Pro Pro Phe Ala Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro 295 Glu Leu Glu Asn Ile Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val 305 310 315 Asn Ser Ile Arg Thr Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala 325 330 Leu Thr Val Ala Arg Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn 340 345 Gln Gly Ile Ser Val Asn Ile 355 <210> 307 <211> 1212 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1189) <223> RXN00528 <400> 307 ttctgctggg aatccccaca ttttggaacg tagcgtcgat aagcgtgcgg cgaagctttt 60 teggtegegg cegttatett tttaagagga gaaattttag atg age aeg tee aec 115 Met Ser Thr Ser Thr atc agg gtt gcc att gcc gga gtc gga aac tgc gcg acc tcc ctc att 163 Ile Arg Val Ala Ile Ala Gly Val Gly Asn Cys Ala Thr Ser Leu Ile 15 cag ggt gtg gaa tat tac cga aat gcg gat cct tcc gaa act gtc ccg 211 Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro Ser Glu Thr Val Pro 25 ggt ttg atg cac gtc aaa ttc ggt gat tac cac gtt ggc gac att gaa 259 Gly Leu Met His Val Lys Phe Gly Asp Tyr His Val Gly Asp Ile Glu 40 ttc gtg gcc gcg ttc gac gtc gac gcc gaa aaa gta ggc atc gat ctt 307 Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys Val Gly Ile Asp Leu gcc gac gcc acc gag gct tca caa aac tgc act atc aaa atc gcc gat 355 Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr Ile Lys Ile Ala Asp 70 75 gtc cca cag acc ggc atc aac gtg ctg cgt ggc ccg act ctc gac ggc 403 Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly Pro Thr Leu Asp Gly 90 95 100 ctg ggc gat cat tac cgc gcg acc atc gac gag tcc acc gcc gag cca 451 Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu Ser Thr Ala Glu Pro 105 110

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							gaa Glu									547
							gcc Ala									595
							gct Ala									643
							aaa Lys									691
	_	_		_	_		ttt Phe 205	_	-	-		_	_	_	_	739
							ggc Gly									787
	_	_		_	-	-	tcc Ser	_	_	-					-	835
							ggt Gly									883
-		-					tcc Ser	-		_				_	_	931
							ctc Leu 285									979
							ctc Leu									1027
							gtt Val									1075
							atg Met									1123
							gac Asp									1171
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Ala Phe Ile Ile Glu Ala 360

<210> 308

<211> 363

<212> PRT

<213> Corynebacterium glutamicum

<400> 308

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Ala Thr Ser Leu Ile Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro 20 25 30

Ser Glu Thr Val Pro Gly Leu Met His Val Lys Phe Gly Asp Tyr His 35 40 45

Val Gly Asp Ile Glu Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys 50 60

Val Gly Ile Asp Leu Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr 65 70 75 80

Ile Lys Ile Ala Asp Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly 85 90 95

Pro Thr Leu Asp Gly Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu 100 105 110

Ser Thr Ala Glu Pro Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys 115 120 125

Ala Asp Val Leu Val Ser Tyr Leu Pro Val Gly Ser Glu Glu Ala Asp 130 135 140

Lys Phe Tyr Ala Gln Ala Ala Ile Asp Ala Gly Cys Ala Phe Val Asn 145 150 155 160

Ala Leu Pro Val Phe Ile Ala Ser Asp Pro Glu Trp Ala Lys Lys Phe 165 170 175

Thr Asp Ala Gly Ile Pro Ile Val Gly Asp Asp Ile Lys Ser Gln Ile 180 185 190

Gly Ala Thr Ile Thr His Arg Val Leu Ala Arg Leu Phe Glu Glu Arg 195 200 205

Gly Val Arg Val Asp Arg Thr Met Gln Leu Asn Val Gly Gly Asn Met 210 220

Asp Phe Lys Asn Met Leu Asp Arg Asn Arg Leu Glu Ser Lys Lys Val 225 230 235 240

Ser Lys Thr Gln Ala Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser 245 250 255

Gly Lys Val Glu Asp Arg Asn Val His Ile Gly Pro Ser Asp His Val . 260 265 270 BGI-126CP - 437 -

Gln Trp Leu Asp Asp Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr 280 Ala Phe Gly Gly Val Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp 295 Asp Ser Pro Asn Ser Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala Lys Ile Ala Leu Asp Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser 325 330 Ser Tyr Leu Met Lys Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala Cys Glu Arg Leu Glu Ala Phe Ile Ile Glu Ala <210> 309 <211> 795 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(772) <223> RXN03057 <400> 309 catcaacqcc qaqtacaact aaqqacaact qataatqaca aatqctqcaa ttqtcqqatq 60 aggagacgtc gcaaccgttc atacagaagc gctggaagct ttg gct tcc gat ctt 115 Leu Ala Ser Asp Leu 1 ggt att aag ttc gtc gca gtg gtg gat aaa gat cta gag act gct gag 163 Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp Leu Glu Thr Ala Glu 10 aaa ttt gcg acg gga ctt gga gct gct ggc gat tct tca gaa agc agc 211 Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp Ser Ser Glu Ser Ser gtc aag gcc cac ggc agc ctg ccg gct ttg ttc tcc aaa aag aag atc 259 Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe Ser Lys Lys Ile 45 gat gtt cta cac atc acc ccc cac gac caa cac att ggt ttg gct 307 Asp Val Leu His Ile Thr Thr Pro His Asp Gln His Ile Gly Leu Ala 60 ctc gaa gcg cta cac cac ggt gta aat gtc atc ctg gaa aag ccg ttg 355 Leu Glu Ala Leu His His Gly Val Asn Val Ile Leu Glu Lys Pro Leu 75 gct aat gag ttg gac cag gcg cag cgt ctc atc gac tac ttg gat gaa 403 Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile Asp Tyr Leu Asp Glu 90 95

aac ccc gat ggt cca aag att gca gtg tgc tat cag aac cgt tac aac

110	Gly Pro 105	Lys Ile	e Ala	Val 110	Cys	Tyr	Gln	Asn	Arg 115	Tyr	Asn	
gtt tcc tcc Val Ser Ser 120												499
gcc atc aat Ala Ile Asn 135			Ser					_				547
tac tac acc Tyr Tyr Thr 150												595
ggc ctg ctg Gly Leu Leu	_	_				_	_	_	_	_		643
ttc ctt gga Phe Leu Gly												691
tat gcc gat Tyr Ala Asp 200												739
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aca												795
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Gln Asn Arg Tyr Asn Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp 125

Ser Gly Asp Leu Gly Ala Ile Asn Gly Ala Tyr Ser Ser Ser Val Val Trp 130

Thr Arg Thr Pro Gly Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln 160

Ala His Ser Gly Gly Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu 175

Asp Leu Leu Gln Trp Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Gly Thr 185

Val Ser Thr Asp Lys Tyr Ala Asp 200

His Ala Tyr Ile Gly His Glu Ser Gly Val His Thr Ser Glu Val Ser

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gct aat gag Ala Asn Glu												403
aac ccc gat Asn Pro Asp												451
gtt tcc tcc Val Ser Ser 120												499
gcc atc aat Ala Ile Asn 135			Ser									547
tac tac acc Tyr Tyr Thr 150												595
ggc ctg ctg Gly Leu Leu	_	_				_	_	_	_	_		643
ttc ctt gga Phe Leu Gly		_	-	_			_			_	-	691
tat gcc gat Tyr Ala Asp 200	-	-	_	-				-				739
cac gag tcc His Glu Ser 215			Ser	-		_	tgaa	ıccat	igc t	atto	ggtgat	792
aca												795
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Leu Ala Ser 1	Asp Leu 5	GIA IIE	ьуs	Phe	10	Ala	val	Val	Asp	Lys 15	Asp	
Leu Glu Thr	Ala Glu 20	Lys Phe	Ala	Thr 25	Gly	Leu	Gly	Ala	Ala 30	Gly	Asp	
Ser Ser Glu 35	Ser Ser	Val Lys	Ala 40	His	Gly	Ser	Leu	Pro 45	Ala	Leu	Phe	
Ser Lys Lys 50	Lys Ile	Asp Val		His	Ile	Thr	Thr 60	Pro	His	Asp	Gln	
His Ile Gly 65	Leu Ala	Leu Glu 70	Ala	Leu	His	His 75	Gly	Val	Asn	Val	Ile 80	

Leu Glu Lys Pro Leu Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile 85 90 95 Asp Tyr Leu Asp Glu Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr 100 105 110

Gln Asn Arg Tyr Asn Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp 115 120 125

Ser Gly Asp Leu Gly Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp 130 135 140

Thr Arg Thr Pro Gly Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln 145 150 155 160

Ala His Ser Gly Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu 165 170 175

Asp Leu Cln Trp Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr 180 185 190

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His Ala Tyr Ile Gly His Glu Ser Gly Val His Thr Ser Glu Val Ser 210 215 220

<210> 313

<211> 831

<212> DNA

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<220>

<221> CDS

<222> (101)..(808)

<223> RXA00251

<400> 313

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Met Lys Lys Ile

1 5

gcg gtc gtt acc gga gcg acc gga ggc atg gga att gag atc gtc aaa $\,$ 163 Ala Val Val Thr Gly Ala Thr Gly Gly Met Gly Ile Glu Ile Val Lys $\,$ 10 $\,$ 15 $\,$ 20

gac ctc tcc cgc gac cac att gtc tac gcc ttg ggc cga aat cca gag 211 Asp Leu Ser Arg Asp His Ile Val Tyr Ala Leu Gly Arg Asn Pro Glu 25 30 35

cat ctg gca gct ctc gca gag atc gag gga gta gag cct atc gag tcc 259 His Leu Ala Ala Leu Ala Glu Ile Glu Gly Val Glu Pro Ile Glu Ser 40 45 50

gat atc gtg aag gaa gtg ttg gaa gag gga ggc gtc gac aag cta aaa 307

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Asp Ile Val 55	Lys Glu	Val Leu 60		Glu	Gly	Gly	Val 65	Asp	Lys	Leu	Lys	
aac ctc gac Asn Leu Asp 70												355
gac acg acc Asp Thr Thr												403
gat ctc aac Asp Leu Asn	-		_		_	_	_			_		451
gcc ctc cgc Ala Leu Arg 120			_	-							-	499
ggc aac gga Gly Asn Gly 135			Asn				_	_	_			547
gcc ctc cgc Ala Leu Arg 150			-		_		_	-	-			595
ggc atc cgc Gly Ile Arg	-	-	_								_	643
ctg caa ggc Leu Gln Gly	_	-						_				691
tac atc gaa Tyr Ile Glu 200												739
gct ggc gaa Ala Gly Glu 215	Thr Thr		Thr	Asn	Val		Val	Arg				787
gaa ctg gcg Glu Leu Ala 230	-	_	-	tctç	igg (ggct	tcct	g gç	jc			831
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Gly Arg Asn		His Leu	Ala		Leu	Ala	Glu	Ile		Gly	Val	

		35					40					45				
Glu	Pro 50	Ile	Glu	Ser	Asp	Ile 55	Val	Lys	Glu	Val	Leu 60	Glu	Glu	Gly	Gly	
Val 65	Asp	Lys	Leu	Lys	Asn 70	Leu	Asp	His	Val	Asp 75	Thr	Leu	Val	His	Ala 80	
Ala	Ala	Val	Ala	Arg 85	Asp	Thr	Thr	Ile	Glu 90	Ala	Gly	Ser	Val	Ala 95	Glu	
Trp	His	Ala	His 100	Leu	Asp	Leu	Asn	Val 105	Ile	Val	Pro	Ala	Glu 110	Leu	Ser	
Arg	Gln	Leu 115	Leu	Pro	Ala	Leu	Arg 120	Ala	Ala	Ser	Gly	Cys 125	Val	Ile	Tyr	
Ile	Asn 130	Ser	Gly	Ala	Gly	Asn 135	Gly	Pro	His	Pro	Gly 140	Asn	Thr	Ile	Tyr	
Ala 145	Ala	Ser	Lys	His	Ala 150	Leu	Arg	Gly	Leu	Ala 155	Asp	Ala	Phe	Arg	Lys 160	
Glu	Glu	Ala	Asn	Asn 165	Gly	Ile	Arg	Val	Ser 170	Thr	Val	Ser	Pro	Gly 175	Pro	
Thr	Asn	Thr	Pro 180	Met	Leu	Gln	Gly	Leu 185	Met	Asp	Ser	Gln	Gly 190	Thr	Asn	
Phe	Arg	Pro 195	Glu	Ile	Tyr	Ile	Glu 200	Pro	Lys	Glu	Ile	Ala 205	Asn	Ala	Ile	
Arg	Phe 210	Val	Ile	Asp	Ala	Gly 215	Glu	Thr	Thr	Gln	Ile 220	Thr	Asn	Val	Asp	
Val 225	Arg	Pro	Arg	Ile	Glu 230	Leu	Ala	Asp	Arg	Lys 235	Asp					
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gag	gtacq	ggt a	agtto	cgtto	cg aq	ggaca	aacgt	: cga	agaaa	aggc	_	att Ile		_		115
				acg Thr 10												163
cag	ccg	gaa	сса	ggc	cta	gat	ata	aaa	ctt	tcc	ccc	caa	gcc	gat	att	211

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Gln	Pro	Glu	Pro 25	Gly	Leu	Asp	Ile	Lys 30	Leu	Ser	Pro	Gln	Ala 35	Asp	Ile	
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					gat Asp											307
					gca Ala 75											355
	_	-	-	_	aga Arg				_			_				403
					cct Pro											451
_	_	_			acg Thr			_					_		_	499 [.]
					cgt Arg											547
	_	-			gac Asp 155	_		-	_	-					_	595
					gca Ala											643
					tcc Ser											691
ttg Leu	gat Asp	tac Tyr 200	gcc Ala	atg Met	act Thr	aag Lys	gcg Ala 205	gca Ala	ttg Leu	aac Asn	aat Asn	ttg Leu 210	tca Ser	aag Lys	ggc Gly	739
					ata Ile											787
					acg Thr 235											835
					ttt Phe											883
					gca Ala											931

979

1008

265 270 275 gcc agc tat gtg gta gga gaa acc ctg gga gtc aca ggt ggg acg ccc Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val Thr Gly Gly Thr Pro 280 285 acc cca tagtcggtac aagcggaatc act Thr Pro 295 <210> 316 <211> 295 <212> PRT <213> Corynebacterium glutamicum <400> 316 Met Ile Ser Leu Leu Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu Lys Gly Arg Lys Ala Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp 105 Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln 180 185 Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn 200 205 Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg 210 215 Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser

235

His Gly Gln Pro Gln Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro $245 \\ 250 \\ 255$

Ile Gly Arg Ala Gly His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe 260 265 270

Leu Ala Ser Asp Glu Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val 275 280 285

Thr Gly Gly Thr Pro Thr Pro 290 295

<210> 317

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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(985)

<223> FRXA02654

<400> 317

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Met Ile Ser Leu Leu

1 5

aat gat cca cgt acg cta ttc ccg aaa gtc gat ccc cca aag caa agc 163 Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser 10 15 20

cag ccg gaa cca ggc cta gat ata aaa ctt tcc ccc caa gcc gat att 211 Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile 25 30 35

ggt ctc tcc agc tat caa gga agt gga agg ctt aag ggc cgc aag gct 259 Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu Lys Gly Arg Lys Ala 40 45 50

ctt att act ggt ggc gat tct ggg att gga gct gcc gta gca atc gct 307 Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala Ala Val Ala Ile Ala 55 60 65

tat gct cgc gag ggg gca gat gtt gcg atc gct tac ttg ccc gaa gaa 355
Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala Tyr Leu Pro Glu Glu
70 75 80 85

caa gcc gat gct gac aga gtg ctc caa gca atc gag gaa aca ggt caa 403 Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile Glu Glu Thr Gly Gln 90 95 100

aaa gct ttt tct ttc cct ggt gat ctc cgt gat cca gaa tac tgt cgc 451 Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp Pro Glu Tyr Cys Arg 105 110 115

tcg ctg gtc caa gag acg gtg aac gct tta ggt ggc cta gac atc ttg 499 Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly Gly Leu Asp Ile Leu

		120					125					130				
	aac Asn 135															547
	gac Asp															595
	cgg Arg	-			_	-				-	_				_	643
	atc Ile															691
_	gat Asp		-	_		_		_	_			_		-		739
_	gca Ala 215	_	_	_			-				-			_	_	787
	ggt Gly				_	_	_			-			_			835
	aaa Lys															883
	cct Pro	_		_	_				_			-		_	-	931
	agc Ser															979
	cca Pro 295	tagt	cggt	tac a	aagc	ggaat	c ac	ct								1008
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Pro	Pro	Lys	Gln 20	Ser	Gln	Pro	Glu	Pro 25	Gly	Leu	Asp	Ile	Lys 30	Leu	Ser	
Pro	Gln	Ala 35	Asp	Ile	Gly	Leu	Ser 40	Ser	Tyr	Gln	Gly	Ser 45	Gly	Arg	Leu	

Lys Gly Arg Lys Ala Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala 50 55 60

Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala 65 70 75 80

Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile 85 90 95

Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp 100 105 110

Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly
115 120 125

Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro 130 140

Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val 150 155 160

Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu 165 170 175

Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln
180 185 190

Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn 195 200 205

Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg 210 215 220

Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser 225 230 235 240

His Gly Gln Pro Gln Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro 245 250 255

Ile Gly Arg Ala Gly His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe 260 265 270

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Thr Gly Gly Thr Pro Thr Pro 290 295

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<211> 1605

<212> DNA

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<223> RXN01049

<400> 319

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aca atg tcc ato Thr Met Ser Ilo	-	-			-	_	163
atg gat att gg Met Asp Ile Gl	Ser Thr Al		Gly Gly				211
ggc tgc cca ato Gly Cys Pro Ilo 40							259
acc ggt gag ggo Thr Gly Glu Gly 55	Val Ser Th						307
atc acc tca gt Ile Thr Ser Va 70		_					355
atc aaa gat cad Ile Lys Asp Gli			_		-		403
tta atc ttg gtc Leu Ile Leu Vai 10	. Asp Gly Gl		Ala Leu				451
tac gcg gat to Tyr Ala Asp Se: 120		_				J	499
atc gat gag aad Ile Asp Glu Ly: 135	-	s Gly Arg			_		547
tcc tac cac cca Ser Tyr His Pro 150			-				595
gag ttc aac aaa Glu Phe Asn Ly:	-				_		643
ttc aaa ctt gca Phe Lys Leu Ala 18	Gly Ile Th		Ala Thr				691
agt ggc att tto Ser Gly Ile Let 200							739
gag cac atc gg Glu His Ile Gly 215		o Ala Leu					787

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_		-			-			_		cca Pro	_					883
										acc Thr						931
_				-	_	-				ccg Pro	_	_		_	_	979
										tcc Ser						1027
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										gaa Glu						1123
		_				-	_	_	_	ttc Phe				-		1171
				-	-			_	_	acg Thr					-	1219
_					-		_		-	ggc Gly	_		_	_		1267
										atg Met 400						1315
										gtc Val						1363
										gac Asp						1411
										acc Thr						1459
										acg Thr						1507

acg cat cag ccg cgc ttt gcg cac cat tac tcc aag gca aga gag ctt 1555 Thr His Gln Pro Arg Phe Ala His His Tyr Ser Lys Ala Arg Glu Leu 470 475 480 ttc gac gcc ctc tac ctc aag ttg gtc tagcttttcg cagtggaacg 1602 Phe Asp Ala Leu Tyr Leu Lys Leu Val 490 cgc 1605 <210> 320 <211> 494 <212> PRT <213> Corynebacterium glutamicum <400> 320 Met Gly Ser Ile Pro Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp Ser Phe Ala Ser Ser Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu Thr Pro Cys Ile Thr Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu Gln Leu Arg Ala Glu Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly 135 Val Cys Leu His Thr Ser Tyr His Pro Ser Arg Leu Leu Trp Leu Lys Thr Glu Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile Gly Glu Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr Ser Ile Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu 200 Asp Leu Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly 210 215 Glu Ile Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp 230 235

Lys Lys Trp Lys His Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro 245 250 255

Asp Gly Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr 260 265 270

Val Ala Val Ala Ala Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro 275 280 285

Ser Val Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser 290 295 300

Arg Asp Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala 305 310 315 320

Val Thr Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu 325 330 335

Val Leu Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe 340 345 350

Phe Ser Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr 355 360 365

Ile Thr Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly 370 375 380

Val Phe Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met 385 390 395 400

Gly Lys Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val 405 410 415

Ser Thr Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp 420 425 430

Thr Pro Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr $435 \hspace{1.5cm} 440 \hspace{1.5cm} 445$

Ala Leu Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr 450 455 460

Pro Pro Phe Gly Thr Thr His Gln Pro Arg Phe Ala His His Tyr Ser 465 470 475 480

Lys Ala Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu Val 485 490

<210> 321

<211> 1134

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1111)

<223> FRXA01049

<400> 321

BGI-126CP

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					tcc Ser 235											835
-		_	_		gaa Glu		_		-			_	-			883
					ctc Leu											931
					atg Met											979
					ctc Leu											1027
					cag Gln 315											1075
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cagt	ggaa	acg o	cgc													1134
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Ile Leu Pro Ser Val Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr 130 135 140 Arg Val Ser Arg Asp Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val 150 155 Gly Arg Ala Val Thr Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn 165 Leu Asp Glu Val Leu Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe Phe Ser Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr Ile Thr Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu 215 Trp Arg Gly Val Phe Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp 230 Glu His Met Gly Lys Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val Ser Thr Asp His Pro Glu Phe Leu Ala Met Leu Ser Asp 265 Ala Leu Asp Thr Pro Val Ile Pro Leu Glu Met Lys Arg Ala Thr Leu 280 Arg Gly Thr Ala Leu Ile Val Leu Glu Gln Leu Glu Pro Gly Gly Thr 295 Arg Ala Thr Pro Pro Phe Gly Thr Thr His Gln Pro Arg Phe Ala His 315

Val

His Tyr Ser Lys Ala Arg Glu Leu Phe Asp Ala Leu Tyr Leu Lys Leu

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					gac Asp								163
					tca Ser								211
	_				aag Lys 45	_	_	_			_		259
					att Ile								307
					att Ile								355
					gtc Val								403
					ggc Gly								451
					cag Gln 125								499
					ggc Gly				-	_	_		547
					ctg Leu		tgaa	aaact	ga q	gttc	gagaa	aa	594
gag													597
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<210> 324

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

. <400> 324

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Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly 20 25 30

Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu 35 40 45

Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp 50 55 60

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Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp 85 90 Ser Phe Ala Ser Ser Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu 100 105 Thr Pro Cys Ile Thr Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu 115 Gln Leu Arg Ala Glu Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly 135 Val Cys Leu His Thr Ser Tyr His Pro Ser Arg Leu Leu Trp 150 <210> 325 <211> 1065 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(1042) <223> RXA00202 <400> 325 ctggcagcag attgtcatcg gttgtgtcat cgcgcttgcg gtgggcttcg atgtcatccg 60 aaacaaaacc tctaagtaat tcctgaaagg aaattttcac atg tac gct cgt aaa 115 Met Tyr Ala Arg Lys ctt att gct ctg tcc gct tct gtc gtt ttg gct ttc agc ttg tct gct 163 Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala Phe Ser Leu Ser Ala 10 tgc aac cgt gaa tct tct ggc acc agc gca gac ggc ggt tct gcg gat 211 Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp Gly Gly Ser Ala Asp ggg tcg atc acc ttg gct ctg tct acc cag acc aac ccg ttc ttt gtg 259 Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr Asn Pro Phe Phe Val 45 cag ctt cgt gat ggt gcc cag gaa aag gct gat gaa ttg ggc gtg acc 307 Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp Glu Leu Gly Val Thr 60 ctc aat gtt cag gat gct tcc gat gac gct gca acg cag gcc aac cag 355 Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala Thr Gln Ala Asn Gln 75 ctc aac aac gct gtc acc acc ggt gct ggc gtg gtg att gtc aac cca 403 Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val Val Ile Val Asn Pro 95 act gat tot gat got gtg gtg cog tog gtg gaa got oto aac cag got 451

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Thr	Asp	Ser	Asp 105	Ala	Val	Val	Pro	Ser 110	Val	Glu	Ala	Leu	Asn 115	Gln	Ala	
	att Ile															499
	tcc Ser 135															547
_	gcc Ala	_	_						-		_			_	_	595
	ggc Gly						_		_	_	-		_			643
	gag Glu															691
	gcc Ala															739
	cag Gln 215	_					_				_			_		787
-	gcg Ala			_		_	_	_		_	_	_		-	_	835
_	atc Ile	-	-			_				-		-	-		_	883
	gat Asp															931
	gca Ala															979
	gaa Glu 295															1027
_	gcg Ala	_		_	tagt	cggo	cga t	gaaa	aagt	ic c	gt					1065

<210> 326

<211> 314 <212> PRT

<213> Corynebacterium glutamicum

<400> 326

Met Tyr Ala Arg Lys Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala 1 5 10 15

Phe Ser Leu Ser Ala Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp 20 25 30

Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr 35 40 45

Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp 50 55 60

Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala 65 70 75 80

Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val \$85\$ 90 95

Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu
100 105 110

Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser 115 120 125

Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly 130 135 140

Gly Ala Gln Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Gly 145 150 155 160

Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp 165 170 175

Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser 180 185 190

Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp 195 200 205

Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe 210 215 220

Ala Glu Asn Asp Glu Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala 225 230 235 240

Arg Ala Gly Glu Asp Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp 245 250 255

Gly Leu Ala Ala Val Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln 260 265 270

Gln Pro Glu Glu Leu Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu 275 280 285

Leu Arg Gly Glu Asp Ala Glu Thr Glu Val Pro Val Glu Val Val Thr 290 295 300

Val Lys Leu Asp Asn Val Ala Asp Phe Lys 305 310

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<211> 1077
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<213> Corynebacterium glutamicum
<220>
<221> CDS
<222> (101)..(1054)
<223> RXN00872
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ccacattcca tcaaaaatga gtgaagggtt gcatcgccac atg act aac ttg acg
                                                                   115
                                             Met Thr Asn Leu Thr
age act cae gaa gte eta get ate gge ege ttg gge gta gat att tae
                                                                   163
Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr
cca ctt caa agt gga gta gga ctg gcc gat gtt caa tct ttc ggc aag
                                                                   211
Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys
tac etc gge gga age gea gea aac gtt tet gtt gea gee gee ege eat
                                                                   259
Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Ala Arg His
         40
gga cac aat tee gea etg etg tee egt gtg gga aat gat eet tte gge
                                                                   307
Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly Asn Asp Pro Phe Gly
gag tac ctg ctt gct gag ctg gag cgt ttg ggc gtg gac aac cag tac
                                                                   355
Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly Val Asp Asn Gln Tyr
                     75
gtt gcc acc gat cag act ttt aag acc cca gtg acc ttc tgt gaa att
                                                                   403
Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val Thr Phe Cys Glu Ile
                 90
ttc cca ccg gat gat ttc cca ctg tac ttc tac cqc gaa cca aag qct
                                                                   451
Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr Arg Glu Pro Lys Ala
ccg gat ctc aat att gaa tcc gca gac gtc agc ctg gac gat gtg cgc
                                                                   499
Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser Leu Asp Asp Val Arg
gaa gcc gat att ttg tgg ttc aca ctc act ggt ttc agt gaa gag cca
                                                                   547
Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly Phe Ser Glu Glu Pro
                        140
age ege gge aca cae ege gag ate ttg act act egt geg aac egt ege
                                                                   595
Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr Arg Ala Asn Arg Arg
                    155
                                        160
cac acc atc ttt gat ctg gac tac cga cca atg ttc tgg gaa tcc cca
                                                                   643
His Thr Ile Phe Asp Leu Asp Tyr Arg Pro Met Phe Trp Glu Ser Pro
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175

gaa gag gcc acc aag cag gcg gaa tgg gcg ttg cag cat tcc acg g Glu Glu Ala Thr Lys Gln Ala Glu Trp Ala Leu Gln His Ser Thr V 185 190 195												
gcg gtt ggc aac aag gaa gaa tgc gaa atc gca gtg ggc gag acc g Ala Val Gly Asn Lys Glu Glu Cys Glu Ile Ala Val Gly Glu Thr G 200 205 210												
cca gag cgc gcg ggc cga gca ctg ttg gaa cgc ggt gtg gag ttg g Pro Glu Arg Ala Gly Arg Ala Leu Leu Glu Arg Gly Val Glu Leu A 215 220 225	-											
atc gtc aag cag gga cct aag ggt gtc atg gcg atg acc aag gac g Ile Val Lys Gln Gly Pro Lys Gly Val Met Ala Met Thr Lys Asp G 230 235 240 2												
acc gta gaa gtt cct ccg ttc ttc gtc gat gtc atc aac ggt ctt g Thr Val Glu Val Pro Pro Phe Phe Val Asp Val Ile Asn Gly Leu G 250 255 260												
gcc ggc gat gca ttc ggc ggc gcg ctg tgc cac ggt ctg ctc tct g Ala Gly Asp Ala Phe Gly Gly Ala Leu Cys His Gly Leu Leu Ser G 265 270 275												
tgg ccg ttg gaa aag gtt ctc cgt ttt gcc aac acc gcg ggt gcg c Trp Pro Leu Glu Lys Val Leu Arg Phe Ala Asn Thr Ala Gly Ala I 280 285 290												
gtg gcg tcc cgt ctt gaa tgc tcc acc gca atg cct act acc gat g Val Ala Ser Arg Leu Glu Cys Ser Thr Ala Met Pro Thr Thr Asp G 295 300 305												
gtg gaa gcc tcc ctc aac cag aaa gtc tgatatgact cctccgatta Val Glu Ala Ser Leu Asn Gln Lys Val 310 315	1074											
tct	1077											
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Gln Ser Phe Gly Lys Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser V 35 40 45	Val											
Ala Ala Ala Arg His Gly His Asn Ser Ala Leu Leu Ser Arg Val G 50 55 60	Gly											
Asn Asp Pro Phe Gly Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu G 65 70 75	Gly 80											

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Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val 85 90 95

Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr 100 105 110

Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser 115 120 125

Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly 130 135 140

Phe Ser Glu Glu Pro Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr 145 150 155 160

Arg Ala Asn Arg Arg His Thr Ile Phe Asp Leu Asp Tyr Arg Pro Met 165 170 175

Phe Trp Glu Ser Pro Glu Glu Ala Thr Lys Gln Ala Glu Trp Ala Leu 180 185 190

Gln His Ser Thr Val Ala Val Gly Asn Lys Glu Glu Cys Glu Ile Ala 195 200 205

Val Gly Glu Thr Glu Pro Glu Arg Ala Gly Arg Ala Leu Leu Glu Arg 210 215 220

Gly Val Glu Leu Ala Ile Val Lys Gln Gly Pro Lys Gly Val Met Ala 225 230 235 240

Met Thr Lys Asp Glu Thr Val Glu Val Pro Pro Phe Phe Val Asp Val 245 250 255

Ile Asn Gly Leu Gly Ala Gly Asp Ala Phe Gly Gly Ala Leu Cys His
260 265 270

Gly Leu Leu Ser Glu Trp Pro Leu Glu Lys Val Leu Arg Phe Ala Asn 275 280 285

Thr Ala Gly Ala Leu Val Ala Ser Arg Leu Glu Cys Ser Thr Ala Met 290 295 300

Pro Thr Thr Asp Glu Val Glu Ala Ser Leu Asn Gln Lys Val 305 310 315

<210> 329

<211> 622

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(622)

<223> FRXA00872

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1 age act cae gaa gte eta get ate gge ege ttg gge gta gat att tae 163 Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr 10 cca ctt caa agt gga gta gga ctg gcc gat gtt caa tct ttc ggc aag 211 Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys 25 tac ctc ggc gga agc gca gca aac gtt tct gtt gca gcc gcc cgc cat 259 Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Ala Arg His 40 gga cac aat tcc gca ctg ctg tcc cgt gtg gga aat gat cct ttc ggc 307 Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly Asn Asp Pro Phe Gly 355 gag tac ctg ctt gct gag ctg gag cgt ttg ggc gtg gac aac cag tac Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly Val Asp Asn Gln Tyr gtt gcc acc gat cag act ttt aag acc cca gtg acc ttc tgt gaa att 403 Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val Thr Phe Cys Glu Ile 90 tte eea eeg gat gat tte eea etg tae tte tae ege gaa eea aag get 451 Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr Arg Glu Pro Lys Ala 105 110 ccg gat ctc aat att gaa tcc gca gac gtc agc ctg gac gat gtg cgc 499 Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser Leu Asp Asp Val Arg 120 125 gaa gcc gat att ttg tgg ttc aca ctc act ggt ttc agt gaa gag cca 547 Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly Phe Ser Glu Glu Pro 135 140 age ege age aca cae ege gag ate ttg act act egt geg aac egt ege 595 Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr Arg Ala Asn Arg Arg 155 cac acc atc ttt gat ctg gac tac cga 622 His Thr Ile Phe Asp Leu Asp Tyr Arq 170 <210> 330 <211> 174 <212> PRT <213> Corynebacterium glutamicum <400> 330 Met Thr Asn Leu Thr Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu 10 Gly Val Asp Ile Tyr Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val 20 Gln Ser Phe Gly Lys Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val

Ala Ala Ala Arg His Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly 55 Asn Asp Pro Phe Gly Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly 80 Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val 85 Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr 100 Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser 115 Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly 130 Phe Ser Glu Glu Pro Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr 145 Arg Ala Asn Arg Arg His Thr Ile Phe Asp Leu Asp Tyr Arg 165 Arg Ala Asn Arg Arg His Thr Ile Phe Asp Leu Asp Tyr Arg 165
Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val 85 90 95 Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr 100 105 120 120 Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser 115 120 Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly 130 140 Phe Ser Glu Glu Pro Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr 145 150 160 Arg Ala Asn Arg Arg His Thr Ile Phe Asp Leu Asp Tyr Arg 165 170

tgg cgt cta acc cca gca gag cgt gcc gct gac ctg gtg aaa cgt atg

Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg Met

aat gtg gaa gaa aaa gcg ggc ctg atg atc atc ggt tcg cac tac ccc

Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr Pro

gga tac tcg cct ttg gcg ccg gag agt gaa ggc aaa gac gcg gaa aag Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu Lys

45

60

40

55

259

307

355

50

70					75					80					85	
_			-	_		cct Pro	_	-	_		_		_		_	403
						acc Thr										451
_		-			-	cgc Arg		_	_				_	_	-	499
	_		-	_		ctt Leu 140	_					_	_	_	_	547
						ttg Leu										595
	-					ctc Leu								_		643
						tgg Trp					-					691
						gag Glu										739
						cac His 220										787
_		-		_		tcc Ser	_								_	835
						tac Tyr										883
			_		_	aat Asn			_				_			931
					_	ctc Leu	_			_						979
						cca Pro 300										1027
						gct Ala										1075

						atg Met									1123
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						cag Gln									1219
_			-			gac Asp 380									1267
						gag Glu									1315
						tcc Ser									1363
						cac His									1411
						gaa Glu									1459
		_		_	_	gaa Glu 460	_	_							1507
_		-	_			aaa Lys	_	_		_		-	_	_	1555
						gct Ala									1603
						tgg Trp									1651
						tcg Ser									1699
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<212> PRT

<213> Corynebacterium glutamicum

<400> 332

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Ala Pro Tyr Glu Asp Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp 35 40 45

Leu Val Lys Arg Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile 50 55 60

Gly Ser His Tyr Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly 65 70 75 80

Lys Asp Ala Glu Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp 85 90 95

Arg Glu Asp Asn Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu 100 105 110

Ala Thr Ser Ser Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr 115 120 125

Leu Ile Val Arg Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr 130 135 140

Asn Ala Val Gln Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val 145 150 155 160

Ala Phe Ala Ser Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe 165 170 175

Gly Val Asn Glu Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu 180 185 190

Gly Leu Ala Ala Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr 195 200 205

Glu Ala Ala Lys Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly 210 215 220

Tyr Met Ala Asp Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly 225 230 235 240

Thr Phe Gly Glu Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val 245 250 255

Val Arg Gly Leu Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr 260 265 270

Thr Ile Lys His Phe Pro Gly Gly Gly Val Arg Leu Asp Gly His Asp 275 280 285

Pro His Phe His Trp Gly Gln Thr Asn Glu Tyr Pro Thr Glu Asp Ala 290 295 300 Leu Gly Lys Tyr His Leu Pro Pro Phe Gln Ala Ala Ile Asp Ala Gly 305 310 315 320

Cys Ala Ser Ile Met Pro Tyr Tyr Ala Arg Pro Met Asn Asn Ser Ala 325 330 335

Asn Gln Leu Asp Gln Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu 340 345 350

Glu Val Ala Phe Ala Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg 355 360 365

Asp Ala Met Gly His Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile 370 375 380

Asp Ala Met Met Trp Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe 385 390 395 400

Ala Ala Val Arg Ala Gly Thr Asp Ile Phe Ser Asp Met Ala Asn 405 410 415

Pro Arg Arg Leu Leu Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser 420 425 430

Glu Leu Asn Gln Pro Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu 435 440 445

Gly Leu Phe Glu Asn Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile 450 455 460

Ile Gly Ala Pro Glu Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp 465 470 475 480

Ser Val Thr Leu Leu Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser 485 490 495

Cys Ser Lys Pro Glu Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp 500 505 510

Arg Arg Gly Ser Thr Thr Ala Gly Ser Ser His Ser Arg Arg Thr Pro 515 520 525

Arg Gly Asn Leu Gly Val Phe Arg Val Arg Ser Arg Ser Cys Asn Arg 530 540

Val Gly Ser Pro 545

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<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1584)

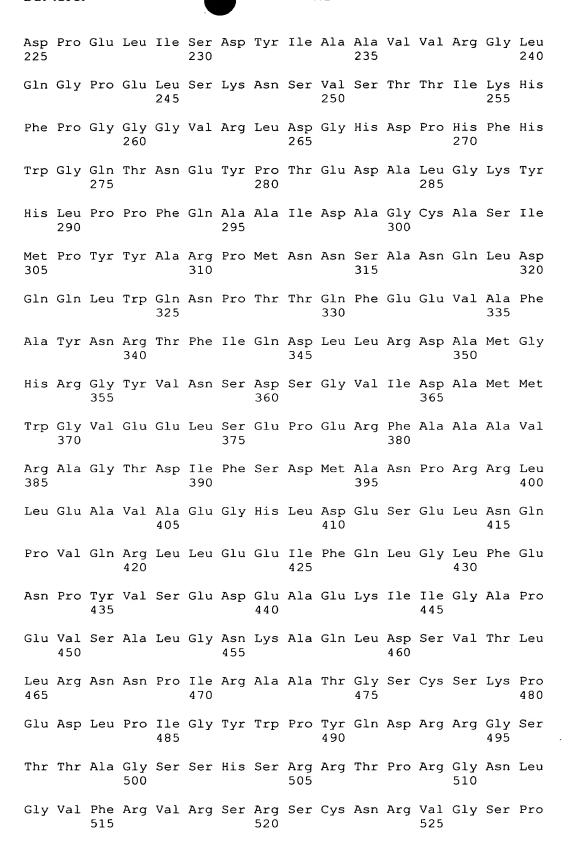
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							gct Ala									912
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			_		-	_	gaa Glu 440	_	_	_						1344
							aaa Lys									1392
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							tgg Trp									1488

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Met Asn Val 35	Glu Glu I	Lys Ala Gly 40		Ile Ile Gly S 45	er His Tyr
Pro Gly Tyr 50	Ser Pro I	Leu Ala Pro 55	Glu Ser	Glu Gly Lys A 60	sp Ala Glu
Lys Cys Glu 65	Pro Leu I	Leu Asn Pro 70	Val Asp	Met Trp Arg G 75	lu Asp Asn 80
Pro Ile Thr	Gly Val I 85	Pro Phe Thr	Glu Pro 90	Val Leu Ala T	nr Ser Ser 95
Thr Glu Asn	Ala Ile A	Asn Leu Arg	Asn Gln 105	Arg Tyr Leu I 1	le Val Arg 10
Asp Asn Leu 115				Trp Thr Asn A 125	la Val Gln
Glu Val Ala 130	Glu Arg S	Ser Arg Leu 135	Gly Ile	Pro Val Ala P 140	ne Ala Ser
Asn Pro Arg 145		Val Ala Leu 150		Gln Phe Gly V	al Asn Glu 160
Ser Ala Gly	Val Phe S 165	Ser Glu Trp	Pro Gly 170	Glu Leu Gly L	eu Ala Ala 175
Leu Arg Asp	Ala Glu I 180	Leu Met Glu	Thr Phe 185	Gly Thr Glu A	la Ala Lys 90
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                                             Met Asn Thr Pro Leu
                                                                   163
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Gln Leu Asn Thr Glu Asn Leu Gln Glu Ile Ala Ser Thr Ser Gly Val
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Gln Ile Pro Ala Phe Asn Arg Ala Asp Val Ala Pro Gly Ile Val His
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Phe Gly Val Gly Gly Phe His Arg Ala His Gln Ala Met Tyr Leu Asn
                                                                   307
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Glu Leu Met Asn Glu Gly Lys Ala Leu Asp Trp Gly Ile Ile Gly Met
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                                                                   355
Gly Val Met Pro Ser Asp Val Arg Met Arg Asp Ala Leu Ala Ser Gln
                                                                   403
gat cac ctt tat acc ctg acc act aaa gct cct gat gga act ctt gat
Asp His Leu Tyr Thr Leu Thr Thr Lys Ala Pro Asp Gly Thr Leu Asp
                 90
caa aaa atc atc gga tcc atc att gac tac gtg ttc gct ccc gag gac
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Gln Lys Ile Ile Gly Ser Ile Ile Asp Tyr Val Phe Ala Pro Glu Asp
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cca qca cgg qcc gtt qca acc ctc gcg cag qac tcc atc cgc att gtt
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Pro Ala Arg Ala Val Ala Thr Leu Ala Gln Asp Ser Ile Arg Ile Val
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                            125
tcc ctc acg gtg act gaa ggc gga tac aac atc gat ccg gcg aca gaa
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Ser Leu Thr Val Thr Glu Gly Gly Tyr Asn Ile Asp Pro Ala Thr Glu
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Asp Phe Asp His Thr Asn Pro Arg Ile Val Ala Asp Arg Glu Ala Leu
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Gln Ala Gly Asp Thr Ser Thr Leu Gln Thr Phe Phe Gly Leu Ile Thr
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_			_		-	_	gat Asp	_		_	_					883
							gaa Glu									931
							ccc Pro 285									979
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	_	_	_		_		gta Val	_	_	_	_		_			1267
							ttg Leu									1315
							tct Ser									1363
cgc	tac	gca	gaa	ggc	acc	gac	gag	cag	ggc	aac	cca	ata	aag	att	gtt	1411

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							gac Asp								gtc Val	1507
							gca Ala								ctt Leu 485	1555
	_	_			_	_	acc Thr		_	_			_	_	_	1603
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Pro Gly Ile Val His Phe Gly Val Gly Gly Phe His Arg Ala His Gln 35 40 45

Ala Met Tyr Leu Asn Glu Leu Met Asn Glu Gly Lys Ala Leu Asp Trp 50 55 60

Gly Ile Ile Gly Met Gly Val Met Pro Ser Asp Val Arg Met Arg Asp 65 70 75 80

Ala Leu Ala Ser Gln Asp His Leu Tyr Thr Leu Thr Thr Lys Ala Pro 85 90 95

Asp Gly Thr Leu Asp Gln Lys Ile Ile Gly Ser Ile Ile Asp Tyr Val 100 105 110

Phe Ala Pro Glu Asp Pro Ala Arg Ala Val Ala Thr Leu Ala Gln Asp 115 120 125

Ser Ile Arg Ile Val Ser Leu Thr Val Thr Glu Gly Gly Tyr Asn Ile 130 135 140

Asp Pro Ala Thr Glu Asp Phe Asp His Thr Asn Pro Arg Ile Val Ala 145 150 155 160

Asp Arg Glu Ala Leu Gln Ala Gly Asp Thr Ser Thr Leu Gln Thr Phe

170 165 175 Phe Gly Leu Ile Thr Ala Ala Leu Ile Ser Arg Lys Glu Ser Gly Ser 185 Thr Pro Phe Thr Ile Met Ser Cys Asp Asn Ile Gln Gly Asn Gly Asp 195 200 Leu Ala Lys Arg Phe Phe Leu Ala Phe Ala His Ser Val Ser Ser Glu 215 Leu Gly Glu Trp Val Glu Asn Asn Val Ala Phe Pro Asn Ser Met Val 225 230 235 Asp Arg Ile Thr Pro Glu Thr Thr Asp Gly Asp Arg Asp Asp Ile Lys Glu Ile Gly Tyr Ile Asp Ala Trp Pro Val Val Ser Glu Asp Phe Thr Gln Trp Val Leu Glu Asp Ala Phe Thr Gln Gly Arg Pro Ala Tyr Glu Glu Val Gly Val Gln Val Val Ser Asp Val Glu Pro Tyr Glu Leu Met Lys Leu Arg Leu Leu Asn Ala Ser His Gln Gly Leu Cys Tyr Phe Gly 310 His Leu Ala Gly His His Met Val His Asp Val Met Ala Asp Thr Arg 325 Phe Gln Asp Phe Leu Leu Ala Tyr Met Glu Arg Glu Ala Thr Pro Thr 345 Leu Lys Glu Leu Pro Gly Val Asp Leu Asp Ala Tyr Arg Arg Gln Leu Ile Ala Arg Phe Gly Asn Ala Ala Val Lys Asp Thr Val Pro Arg Leu 375 Cys Ala Glu Ser Ser Asp Arg Ile Pro Lys Trp Leu Leu Pro Val Val 395 390 Arg Glu Asn Leu Ala Ala Gly Arg Asp Val Thr Leu Ser Ala Ala Ile Val Ala Ser Trp Ala Arg Tyr Ala Glu Gly Thr Asp Glu Gln Gly Asn Pro Ile Lys Ile Val Asp Arg Leu Ser Glu Arg Val Gln Glu Asn Ala Ser Gly Asn Arg Thr Asp Ile Leu Ser Phe Ile Arg Asp Arg Gly Ile 455 Phe Gly Asp Leu Val Asp Ala Glu Pro Phe Thr Lys Ala Tyr Ser Glu 465 475 Thr Leu Ser Ser Leu His Asp Arg Gly Ala Glu Ala Thr Ile Asp Ala 485 490

Leu Leu Thr Gln Val Thr Val 500

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<223> RXA02528

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			1		5	

- agc ctc aag gaa gtt gct gag tta gct gga gtc ggt tat gcc aca gcc 163 Ser Leu Lys Glu Val Ala Glu Leu Ala Gly Val Gly Tyr Ala Thr Ala
- tcg agg gca cta tct ggc aag ggg tat gtg tcc ccg cag acg cgg gag 211 Ser Arg Ala Leu Ser Gly Lys Gly Tyr Val Ser Pro Gln Thr Arg Glu 25 30 35
- aaa gtt cag gcg gct aaa gag ctg aac tat gta cca aat cag ctg 259 Lys Val Gln Ala Ala Lys Glu Leu Asn Tyr Val Pro Asn Gln Leu
 40 45
- gcc aag gcg ttg cgg gaa cat cgc agt gcc ttg gtg ggg gtc att gtt 307 Ala Lys Ala Leu Arg Glu His Arg Ser Ala Leu Val Gly Val Ile Val
- ccg gat ttg tcc aat gag tat tat tcg gaa tcg ctg cag act att cag 355
 Pro Asp Leu Ser Asn Glu Tyr Tyr Ser Glu Ser Leu Gln Thr Ile Gln
 70 80 85
- cag gat ctg aaa gct gct ggc tat caa atg ctg gtt gcg gag gcc aac 403 Gln Asp Leu Lys Ala Ala Gly Tyr Gln Met Leu Val Ala Glu Ala Asn 90 95 100
- agt gtg cag gcg cag gac gtg gtg atg gaa tcg ttg atc tcg att caa 451 Ser Val Gln Ala Gln Asp Val Val Met Glu Ser Leu Ile Ser Ile Gln 105 110 115
- gct gca gga att atc cac gtt cca gtg gtc ggc tca att gct cct gaa 499
 Ala Ala Gly Ile Ile His Val Pro Val Val Gly Ser Ile Ala Pro Glu
 120 125 130
- gga atc ccc atg gtg cag ttg act cgt ggt gaa ttg ggt cct ggt ttc 547 Gly Ile Pro Met Val Gln Leu Thr Arg Gly Glu Leu Gly Pro Gly Phe 135 140 145
- cct cgg gtg ttg tgt gat gat gag gct ggg ttt ttt cag ctg acc gag 595
 Pro Arg Val Leu Cys Asp Asp Glu Ala Gly Phe Phe Gln Leu Thr Glu
 150 165

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_					_	cag Gln	-	_	_				_			691
	_				_	gag Glu		_								739
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	_			_	_	aat Asn	_	_	_			_				883
						gag Glu										931
	_		_		_	cat His			_				-		_	979
_	-	-	-	_		gaa Glu 300			-					_		1027
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Gly Tyr Ala Thr Ala Ser Arg Ala Leu Ser Gly Lys Gly Tyr Val Ser 20 25 30

Pro Gln Thr Arg Glu Lys Val Gln Ala Ala Ala Lys Glu Leu Asn Tyr 35 40 45

Val Pro Asn Gln Leu Ala Lys Ala Leu Arg Glu His Arg Ser Ala Leu 50 55 60

Val Gly Val Ile Val Pro Asp Leu Ser Asn Glu Tyr Tyr Ser Glu Ser 65 70 75 80

Leu Gln Thr Ile Gln Gln Asp Leu Lys Ala Ala Gly Tyr Gln Met Leu 85 90 95

Val Ala Glu Ala Asn Ser Val Gln Ala Gln Asp Val Val Met Glu Ser 100 105 110

Leu Ile Ser Ile Gln Ala Ala Gly Ile Ile His Val Pro Val Val Gly
115 120 125

Ser Ile Ala Pro Glu Gly Ile Pro Met Val Gln Leu Thr Arg Gly Glu 130 135 140

Leu Glý Pro Gly Phe Pro Arg Val Leu Cys Asp Asp Glu Ala Gly Phe 145 150 155 160

Phe Gln Leu Thr Glu Ser Val Leu Gly Gly Ser Gly Met Asn Ile Ala 165 170 175

Ala Leu Val Gly Glu Glu Ser Leu Ser Thr Thr Gln Glu Arg Met Arg 180 185 190

Gly Ile Ser His Ala Ala Ser Ile Tyr Gly Ala Glu Val Thr Phe His 195 200 205

Phe Gly His Tyr Ser Val Glu Ser Gly Glu Glu Met Ala Gln Val Val 210 215 220

Phe Asn Asn Gly Leu Pro Asp Ala Leu Ile Val Ala Ser Pro Arg Leu 225 230 . 235 240

Met Ala Gly Val Met Arg Ala Phe Thr Arg Leu Asn Val Arg Val Pro $245 \hspace{1.5cm} 250 \hspace{1.5cm} 255 \hspace{1.5cm}$

His Asp Val Val Ile Gly Gly Tyr Asp Asp Pro Glu Trp Tyr Ser Phe 260 265 270

Val Gly Ala Gly Ile Thr Thr Phe Val Pro Pro His Glu Glu Met Gly 275 280 285

Lys Glu Ala Val Arg Leu Leu Val Asp Leu Ile Glu Asn Pro Glu Leu 290 295 300

Pro Thr Gly Asp Val Val Leu Gln Gly Gln Val Ile Leu Arg Gly Ser 305 310 315 320

Ser Thr His Ser Gly 325

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_	caa Gln			_		-	_	_						_		835
	g cgc ı Arg															883
	a gga o Gly															931
	c ctg a Leu															979
	c cgc Arg 295		_				_		_	_	-		_	_		1027
	aaa Lys															1075
	gac Asp															1123
	c cca r Pro															1171
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Glu Pro Val Glu Val Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp

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gta gcg ctt tac cga gag cat tcc tat tac aca gca acc cca tgg cga 163 Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr Ala Thr Pro Trp Arg 10 15 20
gga acc tgg gca gcc gat ggc ggt gga gtg ctc atg act caa gcc atc 211 Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu Met Thr Gln Ala Ile 25 30 35
cac tac atc gat ctt ttg tac tgg ctg ttg ggc gaa ccc gtg gaa gtt 259 His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly Glu Pro Val Glu Val 40 45 50
ttc ggc tac acc aac tcc ttc aaa cac ggc gac aac atc gaa gtc gaa 307 Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp Asn Ile Glu Val Glu 55 60 65
gac agc gcc gtt gcc act gtg cgt ttt gaa tcg ggc gcg ttg gcc aca 355 Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser Gly Ala Leu Ala Thr 70 75 80 85
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gtg atg gga Val Met Gly
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Met Thr Gln Ala Ile His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly

35 40 45

Glu Pro Val Glu Val Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp

Asn Ile Glu Val Glu Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser 65 70 75 80

Gly Ala Leu Ala Thr Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu $85\,$, $90\,$ 95

Gly Ala Gln Val Gln Val Met Gly
100

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<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> RXN00310

<400> 343

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Met Ser Asp Lys Ile

1 5

tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc 163
Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile
10 15 20

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gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct 259 Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser 40 45 50

ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att
Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile
55 60 65

gtc gca gtc tgc acc cca cat cca acc cac gaa aca gtg gtc ctc gcc 355
Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala

gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc 403 Ala Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile 90 95 100

gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg 451 Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly 105 110 115

gtc caa ctt ggc gtg ctc ttc cag cgc cgc ttc tgg ccc gcg qct caa 499



Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe Trp Pro Ala Ala Gln 120 125 130

aaa atg aaa aag gag ccg tca tgg gcc aat gca cgg tagcgcttta Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala Arg 135 140 145 545

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558

<210> 344

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 344

Met Ser Asp Lys Ile Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile
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Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val 20 25 30

Ser Ala Val Cys Asp Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala 35 40 45

Lys Tyr Gly Ile Ser Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala 50 55 60

Ser Gly Val Asp Ile Val Ala Val Cys Thr Pro His Pro Thr His Glu 65 70 75 80

Thr Val Val Leu Ala Ala Ala Ala Gly Val His Val Leu Cys Glu 85 90 95

Lys Pro Ile Ala Ile Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala 100 105 110

Cys Glu Ser Ala Gly Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe 115 120 125

Trp Pro Ala Ala Gln Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala 130 135 140

Arg 145

<210> 345

<211> 558

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(535)

<223> FRXA00310

<400> 345

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aaaccqcctt caccaaqctt qaaqatctag ggaagaaata atg tct gac aag atc

Met Ser Asp Lys Ile 1 tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc 163 Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile 211 gaa gca gtt cag gca atc ccc ggc gca gaa gtc agc gca gtc tgt gat Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val Ser Ala Val Cys Asp gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct 259 Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser 45 307 ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile 60 355 gte gca gte tge ace cca cat cca ace cac gaa aca gtg gte ete gee Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala 80 75 403 gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile 90 95 gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg 451 Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly 105 110 499 qtc caa ctt qqc qtq ctc ttc caq cqc cqc ttc tqq ccc qcq qct caa Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe Trp Pro Ala Ala Gln 120 125 aaa atg aaa aag gag ccg tca tgg gcc aat gca cgg tagcgcttta 545 Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala Arg 140 ccgagagcat tcc 558 <210> 346 <211> 145 <212> PRT <213> Corynebacterium glutamicum <400> 346 Met Ser Asp Lys Ile Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val

1 5 10 15

Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val 25

Ser Ala Val Cys Asp Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala 35

Lys Tyr Gly Ile Ser Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala 50

Ser Gly Val Asp Ile Val Ala Val Cys Thr Pro His Pro Thr His Glu

75

65



70



80

Thr Val Val Leu Ala Ala Ala Ala Gly Val His Val Leu Cys Glu 85 90 95

Lys Pro Ile Ala Ile Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala 100 105 110

Cys Glu Ser Ala Gly Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe 115 120 125

Trp Pro Ala Ala Gln Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala 130 135 140

Arg 145

<210> 347

<211> 1342

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1342)

<223> RXA00041

<400> 347

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agctgcgcta gaaacaaaaa ggaaagtagt gtgtggggct atg cac aca gaa ctt 115 Met His Thr Glu Leu 1 5

tcc agt ttg cgc cct gcg tac cat gtg act cct ccg cag ggc agg ctc $$ 163 Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro Pro Gln Gly Arg Leu $$ 10 $$ 15 $$ 20

aat gat ccc aac gga atg tac gtc gat ggc gat acc ctc cac gtc tac 211 Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp Thr Leu His Val Tyr 25 30 35

tac cag cac gat cca ggt ttc ccc ttc gca cca aag cgc acc ggc tgg 259 Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro Lys Arg Thr Gly Trp 40 45 50

gct cac acc acc acg ccg ttg acc gga ccg cag cga ttg cag tgg acg 307 Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln Arg Leu Gln Trp Thr 55 60 65

cac ctg ccc gac gct ctt tac ccg gat gca tcc tat gac ctg gat gga 355
His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser Tyr Asp Leu Asp Gly
70 75 80 85

tgc tat tcc ggt gga gcc gta ttt act gac ggc aca ctt aaa ctt ttc 403 Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly Thr Leu Lys Leu Phe 90 95 100

tac acc ggc aac cta aaa att gac ggc aag cgc cgc gcc acc caa aac 451 Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg Arg Ala Thr Gln Asn

. . .

105 110 115 ctc gtc gaa gtc gag gac cca act ggg ctg atg ggc ggc att cat cgc 499 Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met Gly Gly Ile His Arg 120 125 cgt tcg cct aaa aat ccg ctt atc gac gga ccc gcc agc ggt ttc aca 547 Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro Ala Ser Gly Phe Thr 135 140 ccc cat tac cgc gat ccc atg atc agc cct gat ggt gat ggt tgg aaa 595 Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp Gly Asp Gly Trp Lys 150 155 160 atg gtt ctt ggg gcc caa cgc gaa aac ctc acc ggt gca gcg gtt cta 643 Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr Gly Ala Ala Val Leu 170 tac ege teg aca gat ett gaa aac tgg gaa tte tee ggt gaa ate ace 691 Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe Ser Gly Glu Ile Thr 185 190 ttt gac etc agt gat gea caa eet ggt tet get eet gat etc gtt eec 739 Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala Pro Asp Leu Val Pro 200 ggt ggc tac atg tgg gaa tgc ccc aac ctt ttt acg ctt cgc gat gaa 787 Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe Thr Leu Arg Asp Glu 215 gaa act ggc gaa gat ctc gac gtg ctg att ttc tgt cca caa gga ttg 835 Glu Thr Gly Glu Asp Leu Asp Val Leu Ile Phe Cys Pro Gln Gly Leu 230 235 gac ega ate cae gat gag gtt act cae tae gea age tet gae eag tge 883 Asp Arg Ile His Asp Glu Val Thr His Tyr Ala Ser Ser Asp Gln Cys 250 gga tat gtc gtc ggc aag ctt gaa gga acg acc ttc cgc gtc ttg cga 931 Gly Tyr Val Val Gly Lys Leu Glu Gly Thr Thr Phe Arg Val Leu Arg 265 270 gga ttc agc gag ctg gat ttc ggc cat gaa ttc tac gca ccg cag gtt 979 Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe Tyr Ala Pro Gln Val 280 285 gca gta aac ggt tot gat goo tgg oto gtg ggo tgg atg ggg ctg coo 1027 Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly Trp Met Gly Leu Pro 300 gcg cag gat gat cac cca aca gtt gca cgg gaa gga tgg gtg cac tgc 1075 Ala Gln Asp Asp His Pro Thr Val Ala Arg Glu Gly Trp Val His Cys 310 315 ctg act gtg ccc cgc aag ctt cat ttg cgc aac cac gcg atc tat caa 1123 Leu Thr Val Pro Arg Lys Leu His Leu Arg Asn His Ala Ile Tyr Gln gag ctt ctt ctc cca gag ggg gag tca ggg gta atc aga tct gta tta 1171 Glu Leu Leu Pro Glu Gly Glu Ser Gly Val Ile Arg Ser Val Leu 350

		_	_	_	_	gac Asp 365		_						1219
						gtg Val	_	_	 	-	_	_	_	1267
-					_	tta Leu			 _	_			_	1315
	-		_		_	gga Gly	_							1342

<210> 348

<211> 414

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

Met His Thr Glu Leu Ser Ser Leu Arg Pro Ala Tyr His Val Thr Pro $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Pro Gln Gly Arg Leu Asn Asp Pro Asn Gly Met Tyr Val Asp Gly Asp
20 25 30

Thr Leu His Val Tyr Tyr Gln His Asp Pro Gly Phe Pro Phe Ala Pro 35 40 45

Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln
50 60

Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser 65 70 75 80

Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly 85 90 95

Thr Leu Lys Leu Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg 100 105 110

Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met 115 120 125

Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro 130 135 140

Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp 145 150 155 160

Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr 165 170 175

Gly Ala Ala Val Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe 180 185 190

Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala

195 200 205 Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe 215 Thr Leu Arg Asp Glu Glu Thr Gly Glu Asp Leu Asp Val Leu Ile Phe 225 230 235 Cys Pro Gln Gly Leu Asp Arg Ile His Asp Glu Val Thr His Tyr Ala 250 Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Gly Thr Thr Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr Val Ala Arg Glu 315 Gly Trp Val His Cys Leu Thr Val Pro Arg Lys Leu His Leu Arg Asn His Ala Ile Tyr Gln Glu Leu Leu Pro Glu Gly Glu Ser Gly Val 345 Ile Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val Asp Ile Arg Gly Asn Ile Ser Leu Glu Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala 395 Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly Asp Gly Gln 405 410 <210> 349 <211> 720 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(720) <223> RXA02026 <400> 349 cca ttt cat ata caa cca gaa aca ggt tta tta aat gat ccc aac gga 48 Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly 10 ctt att ttt tat aaa ggg aag tat tat gtt tca cat caa tgg ttc cca 96 Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro 20 25 30

		_	_		ggc Gly		_					_	_	_	144
_					aaa Lys		_						_		192
					ggt Gly 70										240
					atg Met										288
	_			_	cag Gln	_		_	-	_	_	_			336
-	-	-			aag Lys		_		_	_		_			384
					gat Asp							-			432
	_				gca Ala 150				_	_		_			480
					gat Asp								_		528
					gat Asp										576
					caa Gln										624
-					cag Gln						_				672
					att Ile 230										720
)> 35 .> 24														

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly
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Leu Gly Ala Val His Gly Leu Lys Tyr Trp Tyr Asn Tyr Thr Ser Asp 35 40 45

Asp Leu Ile Asn Phe Lys Pro Glu Gly Pro Ile Leu Asn Pro Asp Thr 50 55 60

Lys Tyr Asp Ser His Gly Val Tyr Ser Gly Ser Ala Phe Glu Tyr Asn 65 70 75 80

Gly His Leu Tyr Tyr Met Tyr Thr Gly Asn His Arg Asp Asn His Trp 85 90 95

Gln Arg His Ala Ser Gln Met Ile Ala Arg Leu Lys Glu Asp Gly Ser 100 105 110

Val Glu Lys Phe Pro Lys Pro Val Ile Ser Gln Gln Pro Glu Gly Tyr 115 120 125

Thr Ser His Phe Arg Asp Pro Lys Val Phe Lys Tyr Gly Glu Lys Tyr 130 135 140

Tyr Ala Ile Ile Gly Ala Gln Asn Asn Asp Gln Gln Gly Arg Leu Leu 145 150 155 160

Leu Tyr Asn Thr Glu Asp Ile Ile Asn Trp His Tyr Leu Gly Glu Ile 165 170 175

Asn Thr Glu Leu Asp Asp Phe Gly Tyr Met Trp Glu Cys Pro Asp Tyr 180 185 190

Phe Asn Leu Asp Asn Gln Asp Val Ile Leu Ile Cys Pro Gln Gly Ile 195 200 205

Glu Pro Lys Gly Asn Gln Phe Lys Asn Ile Tyr Gln Ser Gly Tyr Ile 210 215 220

Leu Gly Lys Phe Asp Ile Glu Lys Leu Thr Tyr Glu His Glu Asn Phe 225 230 235 240

<210> 351

<211> 1617

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1594)

<223> RXA02061

<400> 351

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115

agacactggc gtaattgagt gaaggcagga caataaagag atg acg aac gtt tcc

											Met 1	Thr	Asn	Val	Ser 5	
	tat Tyr		_			-				_	-	_		_	_	163
	gca Ala		-		_	_	_	_	-	_	_					211
	cag Gln		_				_									259
	gca Ala 55		_													307
_	cct Pro	_		_	-		_	-	_	_						355
	aac Asn			-								-				403
	act Thr		_	_	_						_				_	451
-	atc Ile		-													499
	gaa Glu 135		_				_			-	-		-		_	547
_	gtt Val					-	-				_	-				595
	gga Gly		_	_		-	-				-	-	_			643
	gtg Val															691
	ctg Leu															739
	gct Ala 215															787
	gat Asp	_			-			_			_		_		_	835

230	235		240	245
			gaa ttc gat gtg Glu Phe Asp Val	-
_	-		ttc tct cgc ccc Phe Ser Arg Pro 275	_
	-		gac ttc gcc cac Asp Phe Ala His 290	
			tcc ccc act gag Ser Pro Thr Glu 305	
		-	att tct ttc cca Ile Ser Phe Pro 320	=
		-	acc cct cca gaa Thr Pro Pro Glu	
			gca ggt tgg acc Ala Gly Trp Thr 355	
	_	-	gtg gcg ttg aag Val Ala Leu Lys 370	_
	-		cgc cac aat cag Arg His Asn Gln 385	_
			ggt gat cca cac Gly Asp Pro His 400	
			ctg ttc att gtc Leu Phe Ile Val	
			ggt tat gta tca Gly Tyr Val Ser 435	
			agc gaa ttt gag Ser Glu Phe Glu 450	
			gaa agt cac ttc Glu Ser His Phe 465	
			gat ctc act gcg Asp Leu Thr Ala 480	

1604 cag ttc gat gaa aac gaa ccg cat gaa ggc cca gtg aga taagagttag Gln Phe Asp Glu Asn Glu Pro His Glu Gly Pro Val Arg 490 495 atgcgttcca gcc 1617 <210> 352 <211> 498 <212> PRT <213> Corynebacterium glutamicum Met Thr Asn Val Ser Gly Tyr His Arg Pro Glu Leu His Ile Thr Ala Glu Ser Gly Val Leu Phe Ala Pro Ala Gly Val Leu Leu Asp Asp Asp Thr Trp His Phe Phe His Gln Tyr Arg Pro Ser Pro Asp His Gly Pro Arg Trp Ala His Gln Phe Ala Glu Arg Thr Pro Phe Val Trp Asp Ile Cys Asp Asp Val Leu Ala Pro Glu Gly Asp Glu Thr Gln Val Arg Ala Gly Ser Val Val Ser Asn Asn Gly Gly Val Asp Leu Tyr Phe Thr Ser Val Val Gly Pro Thr Ser Thr Ile Gln Leu Ala His Ile Asn Asn Ile 105 Arg Gly Thr Thr Glu Leu Ile Asn Glu Asp Glu Leu Gly Leu Asp Pro 120 Asp Val Ser Arg Ile Gly Glu Val Val Gly Asn Thr Asp Gly Tyr Val 135 Lys Phe Arg Ser Pro Cys Val Ile Pro Gly Trp Glu Asp Gln Gly Asn 155 Arg Asp Glu Gly His Ser Gly Trp Leu Met Leu Ala Val Thr Gly Pro Val Glu Ala Pro Thr Val Val Leu Asp Ser Pro Asp Gly Arg Glu Trp Ser Ile Thr Gly Pro Leu Ser Leu Asn Gly Leu Ser Gly Leu Glu Ser Asp Glu Val Leu Val Ala Pro Arg Met Ile Arg Leu Arg Asp Glu 215 Val Asp His Glu Ile Tyr Asp Val Leu Ile Val Thr Ile Glu Gln Asp 225 230 235 Gly Ile Asp Ile Ser Gly Tyr Leu Val Gly Gln Leu Asn Gly Ser Glu 245 250

Phe Asp Val Lys Thr Pro Phe Thr Arg Ile Asp Phe Gly His Asp Phe 260 265 270

Ser Arg Pro Arg Asn Thr Asn Tyr Ala Glu Thr Thr Ile Gly Tyr Asp 275 280 285

Phe Ala His Ile Phe Gly Leu Met Asn Gly Val Gly Arg Leu Asp Ser 290 295 300

Pro Thr Glu His Leu Ser Trp Lys Glu Glu Gly Trp Ala Asn Ala Ile 305 310 315 320

Ser Phe Pro Arg Ile Val Thr Leu Gln Asp Gly Thr Val Phe Gln Thr 325 330 335

Pro Pro Glu Gly Leu Leu Asp Ala Ile His Glu Ser Glu Ala Ala 340 345 350

Gly Trp Thr Gly Leu Cys Glu Ile Pro Ser Asn Ser Ala Val Glu Val 355 360 365

Ala Leu Lys Asp Gln Glu Gly Glu Ile Ala Ala Thr Ile Thr His Arg 370 375 380

His Asn Gln Leu Val Val Asp Arg Ser Met Asn Pro Asn His Ala Gly 385 390 395

Asp Pro His Ala Ile Ala Pro Leu Thr Asp Asp Glu Thr Asp Ser Leu 405 410 415

Phe Ile Val Val Asp Gly Ser Thr Val Glu Val Phe Ala Asp Gly Gly 420 425 430

Tyr Val Ser Met Ala Ser Arg Val Tyr Phe Asn Asn Gly Pro Phe Ser 435 440 445

Glu Phe Glu Val Thr Thr Gly Asp Ala Ser Ile Ile Arg Gln Glu 450 455 460

Ser His Phe Pro Val Asp Phe Ser Ser Val Ser Leu Asp Ile Asp Asp 465 470 475 480

Leu Thr Ala Leu Met Gln Phe Asp Glu Asn Glu Pro His Glu Gly Pro 485 490 495

Val Arg

<210> 353

<211> 1305

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1282)

<223> RXN01369

<400> 353

BGI-126CP - 497 -

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ggc tca ctg cgc Gly Ser Leu Arc			Arg Thr	_		163
ctc aaa ggc gaa Leu Lys Gly Glu 25	Glu Ser Pro				, ,,	211
ttc ggt gcc cad Phe Gly Ala His 40					-	259
aac gaa gtc atc Asn Glu Val Ile 55		Pro Glu Glu				307
gcc gaa gcg ttt Ala Glu Ala Phe 70						355
gcg gga gca ccc Ala Gly Ala Pro	_		_			403
cgt gaa gga tto Arg Glu Gly Phe 105	Ala Arg Glu	_		_		451
ccg aac cgc aac Pro Asn Arg Asr 120			-		-	499
gct ctc acg gas Ala Leu Thr Glu 135		Met Ala Gly				547
acc ctc acc att Thr Leu Thr Ile 150						595
cgc agc atg ctc Arg Ser Met Leu						643
ttt acc acc tgo Phe Thr Thr Trp 185	Ile Thr Ile		-	-		691
gat gcc ctc atc Asp Ala Leu Ile 200				-	-	739
gac gag gac ato Asp Glu Asp Ile 215		Leu Ser His			_	787

	_				_	gtc Val 235		_	_		-	_	_	_			835
				_		ggc Gly	-	_				-	-	_			883
						ggc Gly											931
						gga Gly											979
						gat Asp											1027
	-	_	_	_		gca Ala 315	_					_				-	1075
				_	-	gtt Val	-	-	_		-	_	_	_			1123
	-			_		gtt Val	_	_					_		_	_	1171
	_			_		ctc Leu	-	_	_	_			_	_		-	1219
						acc Thr								-	-	_	1267
				agg Arg		taga	tctt	tt t	agat	taaa	aa to	ca					1305
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	Thr	Leu	Ile	Ala 20	Asp	Leu	Lys	Gly	Glu 25	Glu	Ser	Pro	Ser	Ser 30	Arg	Pro	
	Glu	Ala	Glu 35	Val	Trp	Phe	Gly	Ala	His	Pro	Gly	Ser	Pro	Ser	Thr	Ile	

40

45

35

Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala 50 55 60

Leu Gly Thr Arg Val Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu 65 70 75 80

Leu Lys Ile Leu Ala Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro 85 90 95

Ser Leu Glu Gln Ala Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly 100 105 110

Ile Asp Leu Gly Ala Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys 115 120 125

Pro Glu Leu Ile Val Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe 130 135 140

Arg Pro Leu Arg Asn Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu 145 150 155 160

Pro Leu Asp Arg Tyr Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu 165 170 175

Ser Leu Arg Ala Leu Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys 180 185 190

Arg His Glu Leu Ile Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu 195 200 205

Glu Ala Ser Asp Arg Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile 210 215 220

Ile Glu Leu Asn Glu Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala 225 230 235 240

Leu Leu Leu Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu 245 250 255

Asp Ala Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile 260 265 270

Met Ala Asn Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr 275 280 285

Val Asp Val Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu 290 295 300

Asn Ala Arg Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro 305 310 315 320

Val Pro Ile Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu

Ala Glu Ala Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly 340 345 350

Thr Val Ser Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly 355 360 365

His Ala Ala Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser

370

380

375 Glu Asp Ala Glu Val Phe Leu Ala Arg Val 390 <210> 355 <211> 524 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (1)..(501) <223> FRXA01369 <400> 355 aac gaa cag tgc ctc ggc gat gtc ggc gtt ctg ggt gct ctg ctg ttg 48 Asn Glu Gln Cys Leu Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu aac ttc tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca 96 Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala 20 144 aac ett cae gea tae ate age gge ete gge gta gag ate atg geg aac Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn 192 tee gae aac gtg ete ege ggt gga etg aca tee aaa tae gte gae gte Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val ccg gag ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc 240 Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg 65 gtg gac gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc 288 Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile aac qaa ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc 336 Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala 100 aac cac gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc 384 Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser 115 120 ttg gaa gca ggg gag aag acc ctc gaa gta gca gca ggt cac gcc gca 432 Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala 130 135 tgg gtt cca gca aac gac cca acc att gcg atg cgt tct gag gac gca 480 Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala 145 155 160 150 gaa gta ttc ctc gct agg gtt tagatctttt tagattaaaa tca 524 Glu Val Phe Leu Ala Arg Val 165